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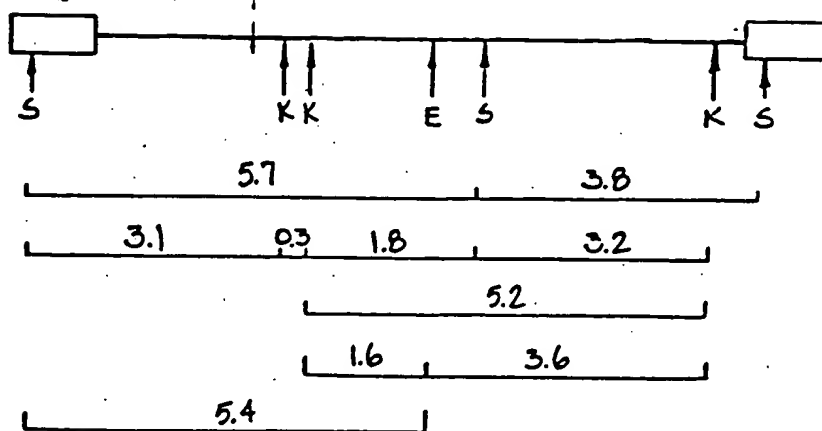


FIG. 1.

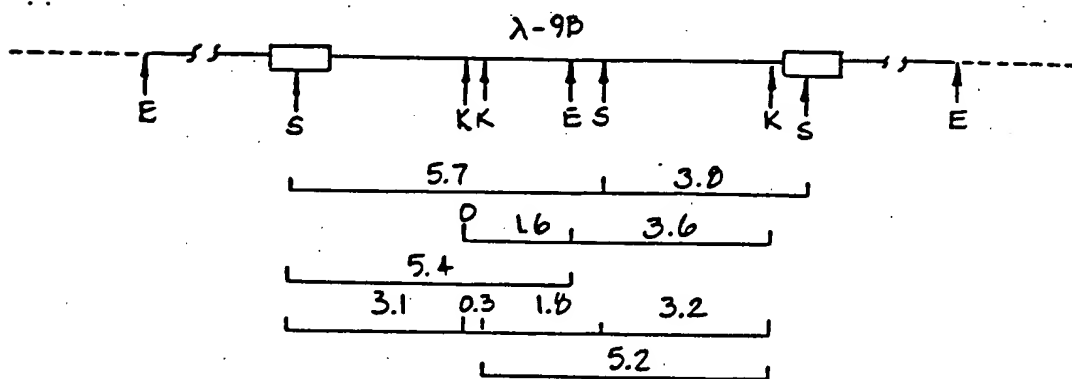


FIG. 2.

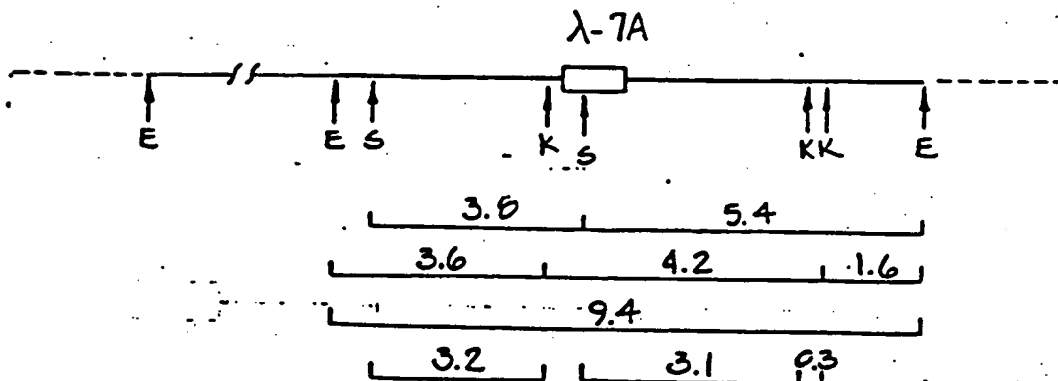


FIG. 3.

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Argument Map in DNA Strand ssarv2
from the '/v/lib/6mers' file.
Translation shown at open reading frames.

FIGURE 4

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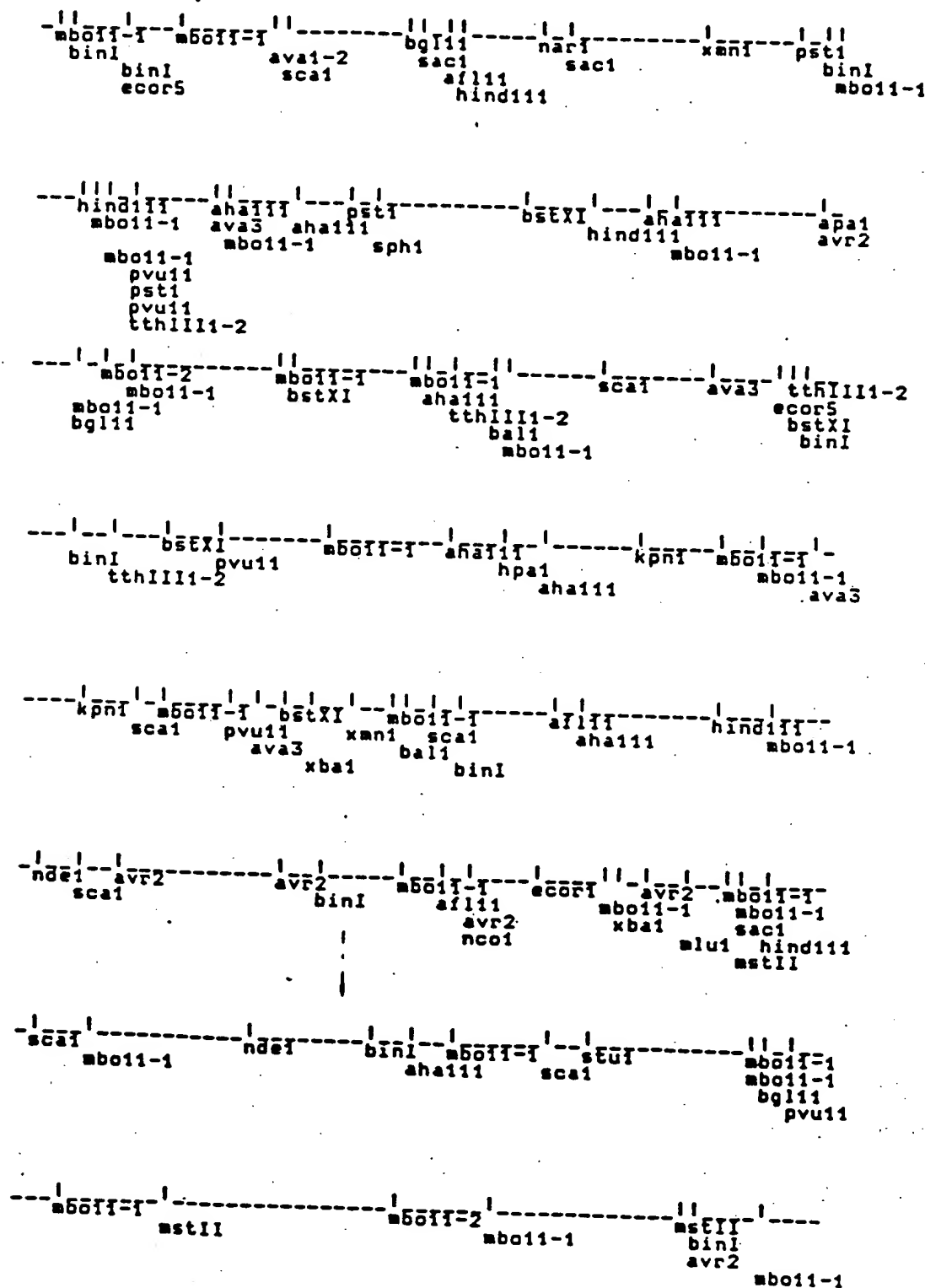
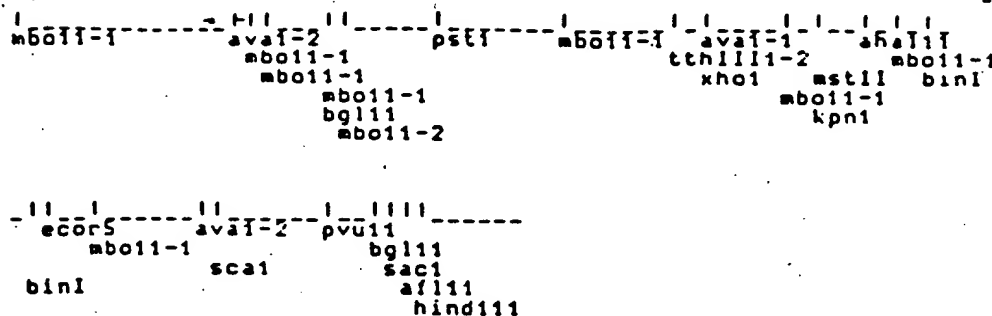


Figure 4
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1 CTGGAAGGGCTAATTTGGTCCCAAGAGACAAGAGATCCTTGATCTGTGGATCTACCACAC
 63 GACCTTCCC6ATTAAACCAGGGTTTCTTCTGTTCTCTAGGAACTAGACACCTAGATGGTGTG
 123 26 mbo11, 50 bin1,
 183 ACAAGGCTACTTCCCTGATTGGCAGAATTACACACCAGGGCCAGGGATCAGATATCCACT
 243 TGTTCCGATGAAGGGACTAACCCTCTTAATGTGTGGTCCCGGTCCCTAGTCTATAGGTGA
 303 107 bin1, 113 ecor5,
 363 GACCTTTGGATGGTGCTTCAAGCTAGTACCAGTTGAGCCAGAGAAGGTAGAAGAGGCCAA
 423 CTGGAACCTACCACGAAGTTCGATCATGGTCAACTCGGTCTCTTCCATCTTCTCCGGTT
 483 172 mbo11,
 543 TGAAGGAGAGAACAACAGCTTGTACACCCTATGAGCCTGCATGGGATGGAGGACGCGGA
 603 ACTTCTCTCTTGTGTGCGAACAATGTGGGATACTCGGACGTACCCTACCTCTGCGCT
 663 296 ava1,
 723 GCTGCATCCGGAGTACTACAAAGACTGCTGACATCGAGCTTTCTACAAGGGACTTTCCGC
 783 CGACGTAGGCCTCATGATGTTTCTGACGACTGTAGCTCGAAAGATGTTCCCTGAAAGGCG
 843 314 sca1,
 903 TGGGGACTTTCAGGGAGGCGTGGGCTGGGCGGGACTGGGGAGTGGCGTCCCTCAGATGC
 963 ACCCTGAAAGGTCCCTCCGACCGGACCCGCCCTGACCCCTCACCAGGGAGTCTACG
 1023 TGCATATAAGCAGACTGCTTTTTGCTGTACTGGGTCTCTCTGTTAGACCAGATCTGAG
 1083 ACGTATATTGCTCTGACGAAAAACGGACATGACCCAGAGAGACCAATCTGGTCTAGACTC
 1143 474 bgl11,
 1203 CCTGGGAGCTCTCTGGCTAACTAGGGAAACCACTGCTTAAGCCTCAATAAGCTTGCCTT
 1263 GGACCTCGAGAGACCGATTGATCCCTTGGGTGACGAATTGAGAGTTATTTGAAACGGAA
 1323 488 sac1, 518 afl11, 532 hind111,
 1383 GAGTGTCTCAAGTAGTGTGTGCGGCTCTGTTGTGTGACTCTGGTAACTAGAGATCCCTCA
 1443 CTCACGAAGTTCATCACACACGGGCAGACAACACACTGAGACCATGATCTCTAGGGAGT
 1503 GACCCCTTTAGTCAGTGTGGAAAAATCTCTAGCAGTGGCGCCCGAACAGGGACGCGAAAG
 1563 CTGGGAAATCAGTCACACCTTTTAGAGATCGTCAACCGCGGGCTTGTCCCTGCGCTTTC
 1623 639 nar1,
 1683 CGAAAGTAGAACCAGAGGAGCTCTCTCGACGAGGACTCGGCTTGTGAAGCGCGCACAG
 1743 GCTTTCATCTTGGTCTCTCGAGAGAGCTGCTCTGAGCCGAACGACTTCGCGCTGTCT
 1803 680 sac1,
 1863 CAAGAGGCGAGGGGCGGCGACTGGTGAAGTACGCCAATTTTTGACTAGCGGAGGCTAGAAG
 1923 GTTCTCCGCTCCCGCGCTGACCACTCATGCGTTAAAACTGATCGCCTCCGATCTTC
 1983 783 MetGlyAlaArgAlaSerValLeuSerGlyGlyGluLeuAspLysTrpGlu
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903 SerArgGluLeuGluArgPheAlaValAsnProGlyLeuLeuGluThrSerGluGlyCys
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TCGTCCCTCGATCTTGCTAAGCGTCAGTTAGGACGGACAATCTTTGTAGTCTTCCGACG

959 pst1,

963 ArgGlnIleLeuGlyGlnLeuGlnProSerLeuGlnThrGlySerGluGluLeuArgSer
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TCTGTTTATAACCTGTGATGTGCGTAGGGAAGTCTGTCTAGTCTTCTTGAATCTAGT

1002 bin1, 1008 mbo11,

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1083 LysGluAlaLeuGluLysIleGluGluGluGlnAsnLysSerLysLysLysAlaGlnGln
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1087 hind111, 1097 mbo11, 1107 mbo11,

1143 AlaAlaAlaAlaAlaGlyThrGlyAsnSerSerGlnValSerGlnAsnTyrProIleVal
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CGTCTCGACGTCGACCGTGTCTTTGTCTGTCGCTGCGGTGCGGTTTAAATGGGATACAC

1147 pvu11, 1150 pst1, 1153 pvu11, 1156 tthIII1,

1203 GlnAsnLeuGlnGlyGlnMetValHisGlnAlaIleSerProArgThrLeuAsnAlaTrp
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GTCTTGGATGTCCCCGTTTACCATGTAGTCCGGTATAGTGGATCTTGAAATTTACGTACC

1250 aha111, 1255 ava3,

1263 ValLysValValGluGluLysAlaPheSerProGluValIleProMetPheSerAlaLeu
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1346 aha111,

1383 AlaAlaMetGlnMetLeuLysGluThrIleAsnGluGluAlaAlaGluTrpAspArgVal
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1451 sph1,

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1563 IleProValGlyGluIleTyrLysArgTrpIleIleLeuGlyLeuAsnLysIleValArg
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TAGGGTCATCTCTTTAGATATTTTCTACCTATTAGGACGTAATTTTATTATCATTCT

1623 MetTyrSerProThrSerIleLeuAspIleArgGlnGlyProLysGluProPheArgAsp
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1683 TyrValAspArgPheTyrLysThrLeuArgAlaGluGlnAlaSerGlnAspValLysAsn
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ATACATCTGGCCAAGATATTTTGAGATTCTCGGCTTGTTCGAAGTGTCTACATTTTTA

1720 hind111,

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Figure 4
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1743 TrpMetThrGluThrLeuLeuValGlnAsnAlaAsnProAspCysLysThrIleLeuLys
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1827 mbo11,

1863 ProGlyHisLysAlaArgValLeuAlaGluAlaMetSerGlnValThrAsnProAlaAsn
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1983 GlyLysGluGlyHisIleAlaLysAsnCysArgAlaProArgLysLysGlyCysTrpArg
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2102 mbo11,

2103 LysIleTrpProSerTyrLysGlyArgProGlyAsnPheLeuGlnSerArgProGluPro
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2104 bgl11, 2141 mbo11,

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2283 AspProSerSerGlnOC
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2342 MetAsnLeuProGlyLysTrpLysProLysMetIle
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2517 mbo11,

2522 AsnLeuLeuThrGlnIleGlyCysThrLeuAsnPheProIleSerProIleGluThrVal
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2627 bal1, 2639 mbo11,

2642 GluLysIleLysAlaLeuValGluIleCysThrGluMetGluLysGluGlyLysIleSer
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2762 ThrLysTrpArgLysLeuValAspPheArgGluLeuAsnLysArgThrGlnAspPheTrp
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2895 ava3,
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2985 ecor5,
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3003 tthIII1, 3006 bstX1, 3021 bin1,
3063 GluProPheArgLysGlnAsnProAspIleValIleTyrGlnTyrMetAspAspLeuTyr
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CTCGGAAATCTTTGTCTTAGGTCTGTATCAATAGATAGTTATGTACCTACTAAACATA
3123 ValGlySerAspLeuGlyIleGlyGlnHisArgThrLysIleGluGluLeuArgGlnHis
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CATCTAGACTGAATCTTTATCCCGTCTGTATCTTGTCTTCTCTTCTGACTCTGTCTGA
3126 bin1, 3171 tthIII1,
3183 LeuLeuArgTrpGlyPheThrThrProAspLysLysHisGlnLysGluProProPheLeu
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3234 bstX1,
3243 TrpMetGlyTyrGluLeuHisProAspLysTrpThrValGlnProIleMetLeuProGlu
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3303 LysAspSerTrpThrValAsnAspIleGlnLysLeuValGlyLysLeuAsnTrpAlaSer
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3308 pvu11,
3363 GlnIleTyrAlaGlyIleLysValLysGlnLeuCysLysLeuLeuArgGlyThrLysAla
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3423 LeuThrGluValIleProLeuThrGluGluAlaGluLeuGluLeuAlaGluAsnArgGlu
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3543 IleGlnLysGlnGlyGlnGlyGlnTrpThrTyrGlnIleTyrGlnGluProPheLysAsn
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3594 sha111,
3603 LeuLysThrGlyLysTyrAlaArgMetArgGlyAlaHisThrAsnAspValLysGlnLeu
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3659 hpa1,

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3663 ThrGluAlaValGlnLysValSerThrGluSerIleValIleTrpGlyLysIleProLys
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 3723 aha111,
 3783 ThrTrpIleProGluTrpGluPheValAsnThrProProLeuValLysLeuTrpTyrGln
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 3835 kpn1,
 3843 LeuGluLysGluProIleValGlyAlaGluThrPheTyrValAspGlyAlaAlaAsnArg
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 4083 GlnProAspLysSerGluSerGluLeuValSerGlnIleIleGluGlnLeuIleLysLys
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 4503 IleProAlaGluThrGlyGlnGluThrAlaTyrPheLeuLeuLysLeuAlaGlyArgTrp
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 4555 mbo11, 4560 bal1,

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4563 ProValLysThrIleHfsThrAspAsnGlySerAsnPheThrSerThrThrValLysAla
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4605 sca1,

4623 AlaCysTrpTrpAlaGlyIleLysGlnGluPheGlyIleProTyrAsnProGlnSerGln
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4639 bin1,

4683 GlyValValGluSerMetAsnAsnGluLeuLysLysIleIleGlyGlnValArgAspGln
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4743 AlaGluHisLeuLysThrAlaValGlnMetAlaValPheIleHisAsnPheLysArgLys
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CGACTTGTGGAATTCGTGTCATGTTACCCTCATAGTAGGTGTTAAATTTTCTTTT

4752 af111, 4791 aha111,

4803 GlyGlyIleGlyGlyTyrSerAlaGlyGluArgIleValAspIleIleAlaThrAspIle
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4863 GlnThrLysGluLeuGlnLysGlnIleThrLysIleGlnAsnPheArgValTyrTyrArg
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4923 AspAsnLysAspProLeuTrpLysGlyProAlaLysLeuLeuTrpLysGlyGluGlyAla
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4956 hind111,

4983 ValValIleGlnAspAsnSerAspIleLysValValProArgArgLysAlaLysIleIle
GTAGTAATACAAGATAATAGTGACATAAAAGTAGTGCCAAGAAGAAAAAGCAAAATCATT
CATCATTATGTTCTATTATCACTGTATTTTCATCACGGTTCTTCTTTTCTTTTATAGTAA

5023 mbo11,

5043 MetGluAsnArgTrpGlnValMetIleValTrpGlnValAspArgMetArgIle
ArgAspTyrGlyLysGlnMetAlaGlyAspAspCysValAlaSerArgGlnAspGluAsp
AGGGATTATGGAAAACAGATGGCAGGTGATGATTGTGTGGCAAGTAGACAGGATGAGGAT
TCCCTAATACCTTTTGTCTACCGTCCACTACTAACACACCGTTTCATCTGCTCTACTCCTA

5103 ArgTreTrpLysSerLeuValLysHisHisMetTyrIleSerLysLysAlaLysGlyTrp
AM
TAGAACATGGAAAAGTTTAGTAAAAACCATATGTATATTTCAAAGAAAGCTAAAAGGATGG
ATCTGTACCTTTTCAAATCATTTGTGGTATACATATAAAGTTTCTTTCGATTTCCTACC

5131 nde1,

5163 PheTyrArgHisHisTyrGluSerThrHisProArgValSerSerGluValHisIle
TTTTATAGACATCACTATGAAAGTACTCATCCAAGAGTAAGTTCAGAAAGTACACATC
AAAAATATCTGTAGTGATACTTTCATGAGTAGGTTCTCATTCAAGTCTTCATGTGTAG

5185 sca1,

5221 ProLeuGlyAspAlaLysLeuValIleThrThrTyrTrpGlyLeuHisThrGlyGluArg
CCCCTAGGGGATGCTAAATTGGTAATAACAACATATTGGGGTCTGCATACAGGAGAAAGA
GGGGATCCCTACGATTTAACCATTATTGTTGTATAACCCCAAGACGTATGTCCTCTTTCT

5223 avr2,

5281 GluTrpHisLeuGlyGlnGlyValAlaIleGluTrpArgLysLysLysTyrSerThrGln
GAATGGCATTGGGGCCAGGGAGTCGCCATAGAATGGAGGAAAAAGAAATATAGCACACAA
CTTACCCTAAACCCGGTCCCTCAGCGGTATCTTACCTCCTTTTTCTTTATATCCTGTGTT

5341 ValAspProGlyLeuAlaAspGlnLeuIleHisLeuHisTyrPheAspCysPheSerGlu
GTAGACCTTGGCTAGCAGACCAACTAATCATCTGCATTATTTGATTGTTTTTCAGAA
CATCTGGGACCGGATCGTCTGGTTGATTAAGTAGACGTAATAAACTAACAAAAAGTCTT

5401 SerAlaIleLysAsnAlaIleLeuGlyTyrArgValSerProArgCysGluTyrGlnAla
TCTGCTATAAAAAATGCCATATTAGGATATAGAGTTAGTCCTAGGTGTGAATATCAAGCA
AGACGATATTTTTTACGGTATAATCCTATATCTCAATCAAGATCCACACTTATAGTTCGT

5440 avr2,

5461 GlyHisAsnLysValGlySerLeuGlnTyrLeuAlaLeuAlaAlaLeuIleThrProLys
GGACATAACAAGGTAGGATCTCTACAATACTTGGCACTAGCAGCATTAAACACCAAAA
CCTGTATTGTTCCATCTAGAGATGTTATGAACCGTGATCGTCETAATTATTGTGGTTT

5476 bin1,

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Figure 4
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5521 LysThrLysProProLeuProSerValLysLysLeuThrGluAspArgTrpAsnLysPro
 AAGACAAAGCCACCTTTGCCTAGTGTAAAGAACTGACAGAGGATAGATGGAACAAGCCC
 TTCTGTTTCGGTGGAACGGATCACAATTCTTTGACTGTCTCCTATCTACCTTGTTCGGG
 5581 GlnLysThrLysGlyHisArgGlySerHisThrMetAsnGlyHisAM
 CAGAAGACCAAGGGCCACAGAGGGAGCCATACAATGAATGGACACTAGAGCTTTTAGAGG
 GTCTTCTGGTTCCGGTGTCTCCCTCGGTATGTTACTTACCTGTGATCTCGAAAATCTCC
 5583 mbo11,
 5641 AGCTTAAGAGAGAAGCTGTTAGACATTTTCTAGGCCATGGCTCCATAGCTTAGGACAAT
 TCGAATTCTCTCTTCGACAATCTGTAAAAGGATCCGGTACCGAGGTATCGAATCCTGTTA
 5643 af111, 5670 avr2, 5676 nco1,
 5701 ATATCTATGAAACTTATGGGGATACCTTGGGCGAGGAGTGGAAAGCCATAATAAGAATTCTGC
 TATAGATACTTTGAATACCCCTATGAACCCGCTCTCACCTTCGGTATTATTCTTAAGACG
 5752 ecor1,
 5761 AACAACTGCTGTTTATTCATTTTCTAGAATTGGGTGTCAACATAGCAGAATAGGCATTATTC
 TTGTTGACGACAAATAAGTAAAGTCTTAACCCACAGTTGTATCGTCTTATCCGTAATAAG
 5821 AACAGAGGAGAGCAAGAAGAAATGGAGCCAGTAGATCCTAATCTAGAGCCCTGGAAGCAT
 TTGTCTCCTCTCGTTCTTCTTTACCTCGGTCTATAGGATTAGATCTCGGGACCTTCGTA
 5836 mbo11, 5862 xba1,
 5881 CCAGGAAGTCAGCCTAGGACTGCTTGTAAACAATTGCTATTGTAAAAAGTGTTCCTTCAT
 GGTCTTCAGTCGGATCCTGACGAACATTGTTAACGATAACATTTTTCACAAACGAAAGTA
 5893 avr2,
 5941 TGCTACGCGTGTTCACAAGAAAAGGCTTAGGCATCTCCTATGGCAGGAAGAAGCGGAGA
 ACGATGCGCACAAAGTGTTCCTTTCCGAATCCGTAGAGGATACCGTCTTCTTCGCTCT
 5945 mlu1, 5988 mbo11,
 6001 CAGCGACGAAGAGCTCCTCAGGACAGTCAGACTCATCAAGCTTCTCTATCAAAGCAGTAA
 GTCGCTGCTTCTCGAGGAGTCTGTGAGTCTGAGTAGTTCGAAGAGATAGTTTCGTCATT
 6008 mbo11, 6011 sac1, 6016 mstII, 6038 hind111,
 6061 GTAGTAAATGTAATGCAATCTTTACAAATATTAGCAATAGTATCATTAGTAGTAGCA
 CATCATTTACATTACGTTAGAAATGTTTATAATCGTTATCATAGTAATCATCATCATCGT
 6121 ATAATAGCAATAGTTGTGTGGACCATAGTACTCATAGAATATAGGAAAATATTAAGACAA
 TATTATCGTTATCAACACACCTGGTATCATGAGTATCTTATATCCTTTTATAATTCTGTT
 6147 sca1,
 6181 AGAAAATAGACAGATTAATTGATAGAATAAGAGAAAAAGCAGAAGACAGTGGCAATGAAA MetLys
 TCTTTTATCTGTCTAATTAACATCTTATTCTCTTTTTCGTCTTCTGTCAACCGTTACTTT ENV
 6222 mbo11,
 6241 ValLysGlyThrArgArgAsnTyrGlnHisLeuTrpArgTrpGlyThrLeuLeuLeuGly
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 CACTTCCCTGGTCTCTTAATAGTCGTGAACACCTCTACCCCGTGGAAACGAGGAACCC
 6301 MetLeuMetIleCysSerAlaThrGluLysLeuTrpValThrValTyrTyrGlyValPro
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 TACAACCTACTAGACATCAGGATGTCTTTTAAACACCCAGTGTCAAATAATACCTCATGGA
 6361 ValTrpLysGluAlaThrThrThrLeuPheCysAlaSerAspAlaArgAlaTyrAspThr
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 CACACCTTTCTTCGTTGATGGTGAGATAAAACACGTAAGTCTACGATCTCGTATACTATGT
 6410 nde1,
 6421 GluValHisAsnValTrpAlaThrHisAlaCysValProThrAspProAsnProGlnGlu
 GAGGTACATAATGTTTGGGCCACACATGCTGTGTACCCACAGACCCCAACCCACAGAA
 CTCCATGTATTACAAACCCGGTGTGTACGGACACATGGGTGTCTGGGGTGGGGTGTCTT
 6481 ValValLeuGlyAsnValThrGluAspPheAsnMetTrpLysAsnAsnMetValGluGln
 GTAGTATTGGGAAATGTGACAGAAAAATTTAACATGTGGAAAAATAACATGGTAGAACAG
 CATCATAAACCTTACACTGTCTTTTAAATTTGTACACCTTTTATTGTACCATCTTGTCT
 6541 MetGlnGluAspIleIleSerLeuTrpAspGlnSerLeuLysProCysValLysLeuThr
 ATGCAGGAGGATATAATCAGTTTATGGGATCAAAGCCTAAAGCCATGTGTAAATTAACC
 TACGTCTCTATATTAGTCAAATACCCCTAGTTTCCGATTTCGGTACACATTTTAATTGG
 6567 binI,

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5601 ProLeuCysValThrLeuAsnCysThrAspLeuGlyLysAlaThrAsnThrAsnSerSer
CCACTCTGTGTTACTTTAAATTGCACTGATTTGGGGAAAGGCTACTAATACCAATAGTAGT
GGTGAGACACAATGAAATTTAACGTGACTAAACCCCTTCGATGATTATGTTATCATCA
6615 sha111,
5661 AsnTrpLysGluGluIleLysGlyGluIleLysAsnCysSerPheAsnIleThrThrSer
AATTGGAAAGAAGAAATAAAGGAGAAATAAAAACTGCTCTTTCAATATCACCACAAAGC
TTAACCTTTCTTCTTTATTTTCTCTTTATTTTGGACGAGAAAGTTATAGTGGTGTTCG
6670 mbo11,
5721 IleArgAspLysIleGlnLysGluAsnAlaLeuPheArgAsnLeuAspValValProIle
ATAAGAGATAAGATTGAGAAAGAAATGCACCTTTTCTGTAACCTTGATGTAGTACCAATA
TATTCTCTATTCTAAGTCTTTCTTTTACGTGAAAAAGCATTGGAACACATCATGTTAT
5781 AspAsnAlaSerThrThrThrAsnTyrThrAsnTyrArgLeuIleHisCysAsnArgSer
GATAATGCTAGTACTACTACCACTATACCACTATAGGTTGATACATTGTAACAGATCA
CTATTACGATCATGATGATGGTTGATATGGTTGATATCCAACATGTAAACATTGTCTAGT
6790 sca1,
5841 ValIleThrGlnAlaCysProLysValSerPheGluProIleProIleHisTyrCysThr
GTCATTACACAGGCCTGTCCAAAGGTATCATTGAGCCAATTCCTACATTATTGTACC
CAGTAATGTGTCCGGACAGGTTTCCATAGTAAACTCGGTTAAGGGTATGTAATAACATGG
6851 stu1,
5901 ProAlaGlyPheAlaIleLeuLysCysAsnAsnLysThrPheAsnGlyLysGlyProCys
CCGGCTGGTTTTGCGATTCTAAAGTGTAAATAATAAACCTTCAATGGAAAAGGACCATGT
GGCCGACCAAAACGCTAAGATTTACATTATTATTTTCAAGTTACCTTTTCTGTTTAC
5961 ThrAsnValSerThrValGlnCysThrHisGlyIleArgProIleValSerThrGlnLeu
ACAAATGTCAAGCAGTACAATGTACACATGGAATTAGGCCAATAGTGTCAACTCAACTG
TGTTTACAGTCTGTCTACCTTACCTTAATCCGGTTATCACAGTTGAGTTGAC
7021 LeuLeuAsnGlySerLeuAlaGluGluGluValValIleArgSerAspAsnPheThrAsn
CTGTTAAATGGCAGTCTAGCAGAAGAAGAGGTAGTAATTAGATCTGACAATTTACGAAC
GACAATTTACCGTCAGATCTCTCTCTCCATCATTAACTAGACTGTTAAAGTGCTTG
7042 mbo11, 7045 mbo11, 7060 bgl11,
7081 AsnAlaLysThrIleIleValGlnLeuAsnGluSerValAlaIleAsnCysThrArgPro
AATGCTAAACCATAAATAGTACAGCTGAATGAATCTGTAGCAATTAAGTGTACAAGACCC
TTACGATTTTGGTATTATCATGCTGACTTACTTAGACATCGTTAATTGACATGTTCTGGG
7102 pvu11,
7141 AsnAsnAsnThrArgLysSerIleTyrIleGlyProGlyArgAlaPheHisThrThrGly
AACAAACAATACAAGAAAAGTATCTATATAGGACCAGGGAGAGCATTTCATACAACAGGA
TTGTTGTTATGTTCTTTTTCATAGATATATCCTGGTCCCTCTCGTAAAGTATGTTGCTCT
7199 mbo11,
7201 ArgIleIleGlyAspIleArgLysAlaHisCysAsnIleSerArgAlaGlnTrpAsnAsn
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TCTTATTATCCTCTATATTCTTTTCTGTGAACATTGTAATCATCTCGTGTACCTATTG
7261 ThrLeuGluGlnIleValLysLysLeuArgGluGlnPheGlyAsnAsnLysThrIleVal
ACTTTAGAACAGATAGTTAAAAATTAAGAGAACAGTTTGGGAATAATAAACAAATAGTC
TGAAATCTTGCTATCAATTTTTTAATCTCTGTCAAACCTTATTATTTTGTATCAG
7321 PheAsnGlnSerSerGlyGlyAspProGluIleValMetHisSerPheAsnCysArgGly
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AAATTAGTTAGGAATCCTCCCTGGGTCTTTAACATTACGTGTCAAATTAACATCTCC
7331 mstII,
7381 GluPhePheTyrCysAsnThrThrGlnLeuPheAsnAsnThrTrpArgLeuAsnHisThr
GAATTTTTTCTACTGTAATACAACACAATGTTTAAATAATACATGGAGGTTAAATCACACT
CTTAAAAAGATGACATTATGTTGTGTTGACAAATTATTATGTACCTCCAATTTAGTGTGA
7441 GluGlyThrLysGlyAsnAspThrIleIleLeuProCysArgIleLysGlnIleIleAsn
GAAGGAACATAAGGAAATGACACAATCATATCCCATGTAGAAATAAAACAAATTATAAAC
CTTCCTTGATTTCTTTTACTGTGTAGTATGAGGGTACATCTTATTTTGTTTAATATTG
7501 MetTrpGlnGluValGlyLysAlaMetTyrAlaProProIleGlyGlyGlnIleSerCys
ATGTGGCAGGAAGTAGGAAAAGCAATGTATGCCCTCCCATTTGGAGGACAAATTAGTTGT
TACACCGTCTTCATCCTTTTCTGTACATACGGGGAGGGTAACCTCCTGTTTAATCAACA
7561 SerSerAsnIleThrGlyLeuLeuLeuThrArgAspGlyGlyThrAsnValThrAsnAsp
TCATCAAATATTACAGGGCTGCTATTAAACAAGAGATGGTGGTACAAATGTAACATAATGAC
AGTAGTTTATAATGTCCCGACGATAATTGTTCTCTACCACCATGTTTACATTGATTACTG

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7621 ThrGluValPheArgProGlyGlyGlyAspMetArgAspAsnTrpArgSerGluLeuTyr
ACCGAGGTCTTCAGACCTGGAGGAGGAGATATGAGGGACAATTGGAGAAGTGAATTATAT
TGGCTCCAGAAGTCTGGACCTCCTCCTCTATACTCCCTGTAACTCTTCACTTAATATA
7628 mbo11,
7681 LysTyrLysValIleLysIleGluProLeuGlyIleAlaProThrLysAlaLysArgArg
AAATATAAAGTAATAAAAAATTGAACCATTAGGAATAGCACCCACCAAGGCAAAGAGAAGA
TTTATATTTTCATTATTTTAACTTGGAATCCTTATCGTGGGTGGTCCGTTTCTCTTCT
7736 mbo11,
7741 ValValGlnArgGluLysArgAlaValGlyIleValGlyAlaMetPheLeuGlyPheLeu
GTGGTGCAGAGAGAAAAAGAGCAGTGGGAATAGTAGGAGCTATGTTCTTGGGTCTTG
CACCACGTCTCTCTTTTTCTCGTCACCCTTATCATCCTCGATACAAGGAACCCAAGAAC
7801 GlyAlaAlaGlySerThrMetGlyAlaValSerLeuThrLeuThrValGlnAlaArgGln
GGAGCAGCAGGAAGCACTATGGGCGCAGTGTCTTACCGCTGACGGTACAGGCCAGACAA
CCTCGTCTCTCTTCTGATACCCGCGTCACAGTAACTGCGACTGCCATGTCCGGTCTGTT
7861 LeuLeuSerGlyIleValGlnGlnGlnAsnAsnLeuLeuArgAlaIleGluAlaGlnGln
TTATTGTCTGGTATAGTGCAACAGCAGAACAAATTTCTGAGGGCTATTGAGGCGCAACAA
AATAACAGACCATATCACGTTGTCTGTTGTTAAACGACTCCCGATAACTCCGCGTTGTT
7921 HisLeuGlnLeuThrValTrpGlyIleLysGlnLeuGlnAlaArgValLeuAlaVal
CATCTGTTGCAACTCACAGTCTGGGGCATCAAGCAGCTCCAGGCAAGAGTCTGGCTGTG
GTAGACAACGTTGAGTGTGAGACCCCGTAGTTCTGTCGAGGTCCGTTCTCAGGACGCAC
7981 GluArgTyrLeuArgAspGlnGlnLeuLeuGlyIleTrpGlyCysSerGlyLysLeuIle
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CTTCTATGAGATTCCCTAGTTGTGAGGATCCCTAAACCCCAACGAGACCTTTTGAGTAA
7989 estII, 7995 binI, 8007 avr2,
8041 CysThrThrAlaValProTrpAsnAlaSerTrpSerAsnLysSerLeuGluAspIleTrp
TGCACCACTGCTGTGCTTGGAAATGCTAGTTGGAGTAATAAATCTCTGGAAGACATTGG
ACGTGGTGACGACACGGAACCTTACGATCAACCTCATTATTTAGAGACCTTCTGTAAACC
8089 mbo11,
8101 AspAsnMetThrTrpMetGlnTrpGluArgGluIleAspAsnTyrThrAsnThrIleTyr
GATAACATGACCTGGATGCACTGGGAAAGAGAAATTTGACAATTACACAAACACAATATAC
CTATTGTACTGGACCTACGTCAACCTTTCTCTTTAACTGTTAATGTGTTTGTATATG
8161 ThrLeuLeuGluGluSerGlnAsnGlnGlnGluLysAsnGluGlnGluLeuLeuGluLeu
ACCTTACTTGAAGAATCGCAGAACCAACAAGAAAAGAATGAACAAGAATTATTAGAATTG
TGAATGAACCTTCTAGCGTCTTGGTTGTTCTTTCTTACTTGTCTTAATAATCTTAAC
8170 mbo11,
8221 AspLysTrpAlaSerLeuTrpAsnTrpPheSerIleThrAsnTrpLeuTrpTyrIleLys
GATAAGTGGGCAAGTTTGTGGAAATGGTTTAGCATAACAACTGGCTGTGGTATATAAAG
CTATTCACCGTTCAAACACCTTAACCAATCGTATTGTTTGACCGACACCATATATTTCT
8281 IlePheIleMetIleValGlyGlyLeuValGlyLeuArgIleValPheAlaValLeuSer
ATATTCATAATGATAGTAGGAGGCTTGGTAGGTTTAAGAATAGTTTTGCTGTGCTTTCT
TATAAGTATTACTATCATCCTCCGAACCATCAAATTCTTATCAAAAACGACACGAAAGA
8341 IleValAsnArgValArgGlnGlyTyrSerProLeuSerPheGlnThrArgLeuProVal
ATAGTGAATAGAGTTAGGCAGGGATACTCACCATTGTCAATTCAGACCCGCTCCAGTC
TATCACTTATCTCAATCCGTCCCTATGAGTGGAACAGTAAAGTCTGGGCGGAGGGTCAG
8400 av1,
8401 ProArgGlyProAspArgProAspGlyIleGluGluGluGlyGlyGluArgAspArgAsp
CCGAGGGGACCCGACAGGCCCCGACGGAATCGAAGAAGAAGGTGGAGAGAGAGACAGAGAC
GGCTCCCTG666CTGTCCG666CTGCTTAGCTTCTTCTTCCACCTCTCTCTCTCTCTG
8431 mbo11, 8434 mbo11,
8461 ArgSerValArgLeuValAspGlyPheLeuAlaLeuIleTrpGluAspLeuArgSerLeu
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TCTAGGCAAGCTAATCACCTACCTAAGAATCGTGAATAGACCTTCTAGACGCCTCGGAC
8503 mbo11, 8505 bg11,
8521 CysLeuPheSerTyrArgArgLeuArgAspLeuLeuLeuIleAlaAlaArgThrValGlu
TCCCTCTTCAGCTACCGCCGCTTGAGAGACTTACTCTTGATTGCAGCGAGGACTGTGGAA
ACGGAGAAGTCTGATGGCGGCAACTCTCTGAATGAGAACTAACGTCGCTCCTGACACCTT
8525 mbo11,

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8581 IleLeuGlyHisArgGlyTrpG...AlaLeuLysTyrTrpTrpSerLeuLeuGlnTyrTrp
ATTCTGGGGGCACAGGGGGTGGGAAGCCCTCAAATATTGGTGGAGTCTCCTGCAGTATTGG
TAAGACCCCGTGTCCCCACCCCTTCGGGAGTTTATAACCACCTCAGAGGACGTCATAACC
8629 pst1,
8641 IleGlnGluLeuLysAsnSerAlaValSerTrpLeuAsnAlaThrAlaIleAlaValThr
ATTGAGGAACATAAGAAATAGTGTCTGTTAGCTGGCTCAACGCCACAGCTATAGCAGTAACT
TAAGTCCTTGATTCTTATCAGGACAATCGACCGAGTTGCGGTGTCGATATCGTCATTGA
8701 GluGlyThrAspArgValIleGluValAlaGlnArgAlaTyrArgAlaIleLeuHisIle
GAGGGGACAGATAGGGTTATAGAAGTAGCACAAGAGCTTATAGAGCTATTCTCCACATA
CTCCCTGTCTATCCCAATATCTTCATCGTGTCTTCTCGAATATCTCGATAAGAGGTGTAT
8761 HisArgArgIleArgGlnGlyLeuGluArgLeuLeuLeuOC MetGlyGlyLysTrpSer
CATAGAAGAAATTAGACAGGGCTTGGAAAGGCTTTTGCTATAAGATGGGTGGCAAGTGGTCA
GTATCTTCTTAATCTGTCCCGAACCTTTCGAAAACGATATTCTACCCACCGTTCACCACT
8765 mbo11,
8822 LysArgSerMetGlyGlyTrpSerAlaIleArgGluArgMetArgArgAlaGluProArg
AAACGTAGTATGGGTGGATGGTCTGCTATAGGGGAAAGAAATGAGACGAGCTGAGCCACGA
TTTGCATCATACCCACCTACCAGACGATATTCCCTTTCTTACTCTGCTCGACTCGGTGCT
8882 AlaGluProAlaAlaAspGlyValGlyAlaValSerArgAspLeuGluLysHisGlyAla
GCTGAGCCAGCAGCAGATGGGGTGGGAGCAGTATCTCGAGACCTGGAAAAACATGGAGCA
CGACTCGGTGCTGCTACCCCAACCTCGTCATAGAGCTCTGGACCTTTTGTACCTCGT
8883 tthIII1, 8916 ava1 xho1,
8942 IleThrSerSerAsnThrAlaAlaThrAsnAlaAspCysAlaTrpLeuGluAlaGlnGlu
ATCACAAGTAGCAATACAGCAGCTACTAATGCTGATTGTGCTGGCTAGAGCACAAGAG
TAGTGTTCATCGTTATGTCTGTCGATGATTACGACTAACACGGACCGATCTTCGTGTTCTC
9002 GluGluGluValGlyPheProValArgProGlnValProLeuArgProMetThrTyrLys
GAGGAAGAGGTGGGTTTCCAGTCAGGTCAGGTACCTTTAAGACCAATGACTTACAAG
CTCCTTCTCCACCCAAAGGTGAGTCTGGAGTCTCATGGAAATTCTGGTTACTGAATGTT
9005 mbo11, 9029 mstII, 9034 kpnI,
9062 AlaAlaLeuAspIleSerHisPheLeuLysGluLysGlyGlyLeuGluGlyLeuIleTrp
GCAGCTTTAGATATTAGCCACTTTTAAAGAAAAGGGGGGACTGGAAGGGCTAATTGG
CGTCGAAATCTATAATCGGTGAAAAATTTTCTTTTCCCCCTGACCTTCCCGATTAAACC
9085 aha111,
9122 SerGlnArgArgGlnGluIleLeuAspLeuTrpIleTyrHisThrGlnGlyTyrPhePro
TCCCAAAGAGAGCAAGAGATCCTTGATCTGTGGATCTACCACACACAAGGCTACTTCCCT
AGGGTTTCTTCTGTTCTCTAGGAAGTAGACACCTAGATGGTGTGTGTTCCGATGAAGGGA
9129 mbo11, 9153 bniI,
9182 AspTrpGlnAsnTyrThrProGlyProGlyIleArgTyrProLeuThrPheGlyTrpCys
GATTGGCAGAATTACACACAGGCGCAGGGATCAGATATCCACTGACCTTTGGATGGTGC
CTAACCGTCTTAATGTGTGGTCCCGTCCCTAGTCTATAAGTGAAGTGAAGAACCTACCACG
9210 bniI, 9216 ecor5,
9242 PheLysLeuValProValGluProGluLysValGluGluAlaAsnGluGlyGluAsnAsn
TTCAAGCTAGTACAGTTGAGCCAGAGAAGGTAGAAGAGGCCAATGAAGGAGAGAACAAC
AAGTTCGATCATGGTCAACTCGGTCTCTTCCATCTTCTCCGGTACTTCTCTCTTGTG
9275 mbo11,
9302 SerLeuLeuHisProMetSerLeuHisGlyMetGluAspAlaGluLysGluValLeuVal
AGCTTGTACACCCCTATGAGGCTGCATGGGATGGAGGACGCGGAGAAAGAAAGTGTAGTG
TCGAACAATGTGGGATACTCGGACGTACCTACCTCCTGCGCCTCTTCTTCAACATCAC
9362 TrpArgPheAspSerLysLeuAlaPheHisHisMetAlaArgGluLeuHisProGluTyr
TGGAGGTTTGACAGCAAACTAGCATTTCATCACATGGCCCGAGAGCTGCATCCGGAGTAC
ACCTCCAAACTGTGCTTTGATCGTAAAGTAGTGTACCGGGCTCTCGACGTAAGGCTCATG
9399 ava1, 9417 sca1,
9422 TyrLysAspCysOP
TACAAAGACTGCTGACATCGAGCTTTCTACAAGGGACTTTCCGCTGGGGACTTTCCAGGG
ATGTTTCTGACGACTGTAGCTCGAAAGATGTTCCCTGAAAGGCGACCCCTGAAAGGTCCC
9482 AGGCGTGGGCTGGGCGGGGACTGGGGAGTGGCGTCCCTCAGATGCTGCATATAAGCAGCTG
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9536 pvu11,

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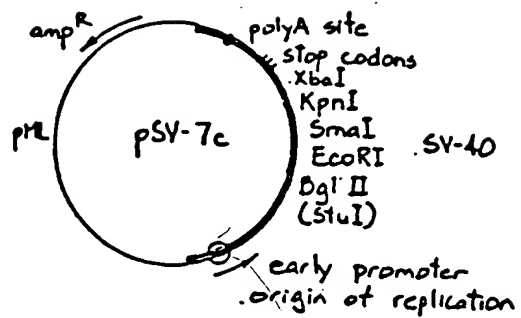
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9542 CTTTTTGCCTGTACTGGGTCTC...GGTTAGACCAGATCTGAGCCTGGGAGC...TCTGGC
GAAAAACGGACATGACCCAGAGAGACCAATCTGGTCTAGACTCGGACCCTCGAGAGACCG
9576 bgl111, 9590 sac1,
9602 TAACTAGGGAACCCACTGCTTAAGCCTCAATAAAGCTTGCCTTGAATGCTTCAAGTAGTG
ATTGATCCCTTGGGTGACGAATTCGGAGTTATTTGAAACGGAACCTCACGAAGTTCATCAC
9620 af1111, 9634 hind111,
9662 TGTGCCCCTCTGTTGTGTGACTCTGGTAACTAGAGATCCCTCAGACCCTTTTGTAGTCAGTG
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9722 TGGAAAAATCTCTAGCA6
ACCTTTTTAGAGATCGTC

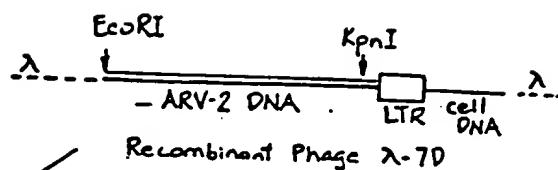
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FIGURE 5
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digestion with
KpnI and EcoRI



digestion with
EcoRI and KpnI

ligation

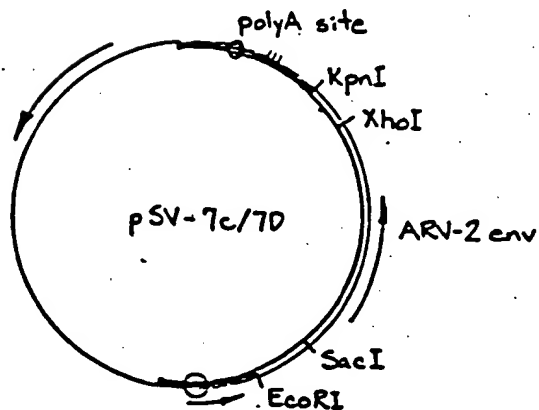
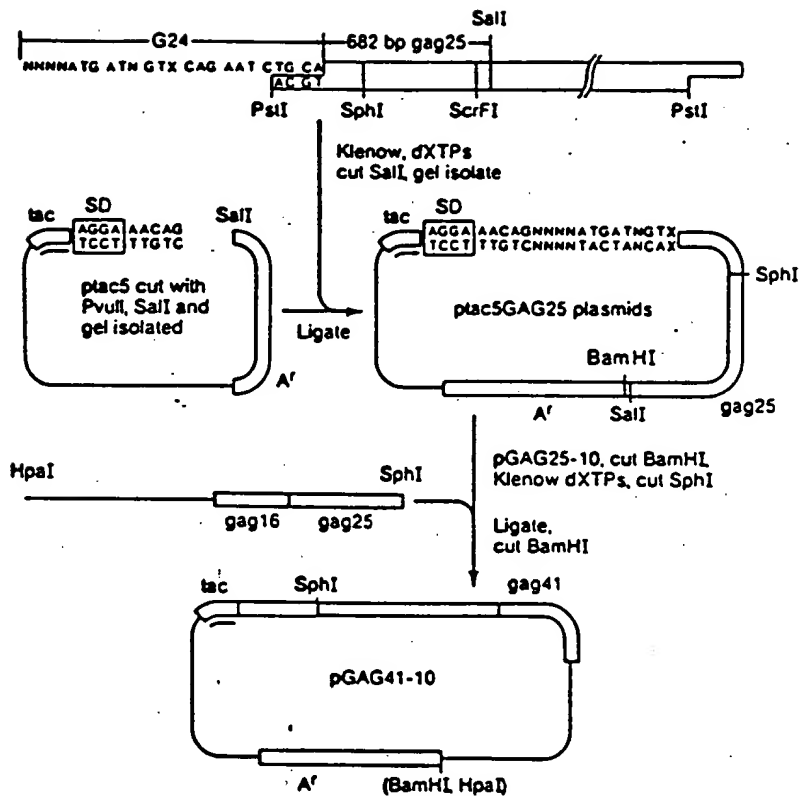


FIG. 6.

Figure 7

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8
F/G.

	ptac 5 Promotor	ptac 5
748	01Anleu01n01g1y01MotvAlM101nAl101SePr0Ar9ThrLeuAn0101TpP0rV01l101P0r0tPh0SeArAl01eW 181 CAGAA1C1G0AGG66CNAATG6TACATCAGG6CA1AT1CACC1TAGAC1TTAAAT6CCTAG6TAAAGTACAGAAAG6CTTTCAC6CCACAA6TAAATACCA1G1TTTCACAGTTA	
808	Se01u01yAl01ThrPr01n01n01pLeuAn01ThrM0tLeuAn01ThrV01G1yM101nAl101M0tG1nM0tLeuLys01u01Thr1101An01G1u01G1nAl101G1u01ThrP0r0Ar9V01 221 TCAGAAAG6CACC6CCACAAAGATTAAACACCATCTAAACACATG6G6G6GACATCAACAGGCA1T6CAAA1T6T1TAAAG6ACATATCAAT6TAAAG6AACT6CAGAA1T6GATACAGTC	
908	M10Pr0V01M101G1yP0r101Al01P0r01yG1nM0tArg01u01P0rArg01ySeArP0r01l01Al01G1yThrSeThrLeuG1nG1u01n1101G1yThrP0rThrAnAn01n01P0rP0 261 CATCCAGT6CAT6CAGG6CCTATTG6CACCAGG6CCAAATG6CAGAGAACCAAGG6GAAGT6CAATACG6AGAACTACTAGCTTACGGAACAAATAGG6T6GAT6CAGCAATATATCCACT	
11108	110Pr0V01G1y01l101Ty01y1yAr9Tp01l01l01Leu01yL0uAn01y1101V01ArgM0tY0rSePr0rThrSeR1101eWAn01p101ArgG1nG1yP0r01yG1u01P0rPh0Ar9V01 301 ATCCAGTAA6G6GAAATCTATAAAGATG6CATATCTCGGATTAATATAAATAGTAAAGATGTATAGCTTACCAGCATCTCGGACATAG6CAACAGG6CNAAG6AACTTTAGAGAT	
12128	TpP01An0Ar9P0r0TpP01y0ThrLeuAr9P0r01G1nAl01SeR1nAn01pV01LysAn01TpM0tThrG1u01ThrLeuL0uV01G1nAnAl01An01P0r0Ar9P0rCys01yThr1101L0uLys 341 TATGTAGAC6G1TCTATAAAGCTCTAAAG6CCGACAAAGCTTCAACAGGATCTAAAAAATTTGGAT6CAGAGAACTTGTGGTCCAAAATG6CAACCCAGATTT6TAGACTATTTTAAA	
13108	Al01eW01yP0r01Al01ThrLeuG1nG1u01M0tM0tThrAl01CysG1nG1yV01G1yG1yP0r01yM101y1yAl01Ar9V01eW 01Stop GCATTC6G6CACCAGCAGCTACACTAGAGAAATGATGACAGCATGTCAGGAGTGGGGGGGAGCCCGG6CATAAAGCAAGACTTTTCGATAG	ptac 5

dtac 5

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FIG. 9

101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000

G A G

P O L

Plac 5 Promoter

Plac 5

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Figure 10

ARV GAG p16 - synthetic Parts A and B

5' ^{arv 234} MetGlnArgGlyAsnPheArg^{5'}AsnGlnArgLysThrValLysCysPheAsnCysGlyLys
 TATTATGCAAAGAGGTAACCTTCAGGAATCAAAGAAAGACCGTTAAGTGTTCACACTGTGGTAAG
 ATAAATACGTTTCTCCATTGAAGTCCTTAGTTTCTTTCTGGCAATTACAAAAGTTGACACCATTG
 3' ^{arv 235}
 10 mnl1, 23 hinf1, 5'
 63 GluGlyHisIleAlaLysAsnCysArgAlaProArgLysLysAlaCysTrpArgCysGly
 GAAGGTCACATCGCTAAGAACTGTAGAGCTCCAAGAAAGAAGGCTTGTGGAGATGTGGT
 CTTCCAGTGTAGCGATTCTTGACATCTCGAGGTTCTTTCTCCGAACAACCTCTACACCA
 76 dde1, 88 ban2 hgiA hgiJ11 sac1 sduI, 89 alu1,
 123 ArgGluGlyHisGlnMetLysAspCysThrGluArgGlnAlaAsnPheLeuGlyLysIle
 AGAGAAGGTCACCAAATGAAGGACTGTACCGAAAGACAAGCTAACTTCTTGGGTAAGATC
 TCTCTTCCAGTGTTTACTTCTGACATGGCTTTCTGTTCGATTGAAGAACCCATTCTAG
 129 bstE2, 131 hph, 148 rsa1, 161 alu1, 178 bgl11 xho2, 179
 sau3a,
 183 TrpProSerTyrLysGlyArgProGlyAsnPheLeuGlnSerArgProGluProThrAla
 TGGCCATCTTACAAGGGTAGACCAGGTAACCTTCTTGCAATCCAGACCAGAACCAACCGCT
 ACCGGTAGAATGTTCCCATCTGGTCCATTGAAGAACGTTAAGTCTGGTCTTGGTTGGCGA
 183 bal1 cfr1 hae1, 184 hae111, 199 acc1, 204 apy1 ecor11 sc
 rF1,
 243 ProProGluGluSerPheArgPheGlyGluGluLysThrThrProSerGlnLysGlnGlu
 CCACCTGAAGAAAGTTTTCAGGTTCCGGTGAAGAAAAGACCACCCCATCTCAAAAGCAAGAA
 GGTGGACTTCTTTCAAAGTCCAAGCCACTTCTTTTCTGGTGGGGTAGAGTTTTCTGTTCTT
 249 mbo11, 267 hph, 270 mbo11,
 303 ProIleAspLysGluLeuTyrProLeuThrSerLeuArgSerLeuPheGlyAsnAspPro
 CCAATCGACAAGGAATTGTACCCATTGACCTCTTTGAGATCCTTGTTCGGTAACGATCCC
 GGTTAGCTGTTCTTAAATGAGGTAACCTGGAGAAACTCTAGGAACAAGCCATTGCTAGGG
 307 taq1, 320 rsa1, 331 mnl1, 339 xho2, 340 sau3a, 357 sau3a
 , 361 mnl1, 362 avai xho1,
 363 SerSerGlnOP AM
 TCGAGCCAATGATAG
 AGCTCGGTTACTATCAGCT
 363 taq1, 377 acc1 hind11 sal1

W Z Y

FIG. 11

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E N V

MetSerArgIleAspCysSerAlaThrGluValLeuIrrValThrValIrrThrGluValProVal 51
ATBCTAGAAATCATGTAGTGTACAGAAATTTGGGTACACATTTATTATGAGTACCTGTG

TrpLysGluValThrThrLeuPheCysAlaSerAspAlaArgAlaIrrAspThrGluValIrrAspThrGluValProVal 91
TGGAAAGAACCACTACCTCTATTTTGTGTCATCAGATGCTAGACATATGATACAGAGGTACATATGTTTGGGCACACATGCTGTATCCACACAGCCCAACCCACAGAGATG

ValLeuGluValThrGluValAsnPheAsnMetTrpLysAsnAsnMetValGluMetGluValIrrSerLeuIrrAspGluValProVal 131
GTATTGGGAAATGTACACAAAATTTAACATGTGAAAATTAACATGTCACAGATGTCAGAGGATATATATCAGTTTATGGCATCAAGGCTAAAGGCTGTGTAAATTAACCCCA

LeuCysValThrLeuAsnCysThrAspLeuGluValIrrAsnThrAsnSerSerAsnTrpLysGluValIrrSerLeuIrrAspGluValProVal 171
CTCTGTGTACTTTAAATTGCACTGATTTGGGAAAGGCTACTAATACCAATAGTAGTAATTCGAAAGAGAAATAAAGGAGAAATTAAGAACTGCTCTTTCAATATATCACCACAGCATG

ArgAspLysIrrGluValIrrAsnAlaLeuPheArgAsnLeuAspValIrrProIrrAspAsnAlaSerThrThrThrAsnIrrThrAsnIrrArgLeuValIrrMetCysAsnAspSerVal 211
AGAGATAAGATTCAGAAAGAAATGCACTTTTTCGTACCTTCATGCTAGTACCAATAGATATGCTAGTACTACTACCAATATACCACTATACCACTATAGGTTTGTATCATTTGTAAACAGATCAGTC

IrrThrGluAlaCysProLysValSerPheGluProIrrProIrrMetIrrCysThrProAlaGluPheAlaIrrLeuLysCysAsnAsnLysThrPheAsnGluLysGluProCysThr 251
ATTACACAGGCTTCCCAAGGATATCATTTGAGCCATTTCCCATACATATTTGACCCGCGCTGTTTCCGATTTCAAGCTGTATATTAAGCTTCAATGGAAGAGGACCATGTACA

AsnValSerThrValGluCysThrMetIrrGluValIrrArgProIrrValIrrSerThrGluValLeuValIrrSerLeuValGluValIrrValIrrSerArgAspAsnPheThrAsnAsn 291
AATGTCAGCAGATACATGTACATGGAATTAGGCCAATAGTGTCACTCACTGCTTAAATGCGAGCTAGCAGAAAGAGGCTAGTAATTAGATCTGACAAATTTCCAGCAACAT

AlaLysThrIrrLeuValIrrLeuAsnLysSerValIrrAlaIrrAsnCysThrArgProAsnAsnThrArgLysSerIrrIrrGluValIrrProGluValIrrPheMetIrrThrGluValArg 331
GCTAAACCATATAGTACAGCTGATGAAATCTGTAGCAATTAACGTACAGAGCCCAACACATACAGAGAAAGATATATAGGACAGGAGAGCATTTTCATACAGAGAGAGA

IrrLeuValIrrAspLysAlaMetCysAsnIrrSerArgAlaGluIrrAsnThrLeuGluValIrrValIrrLysLysLeuValIrrGluValIrrPheGluValIrrValIrrPhe 371
ATAATAGGAGATATAGAAAGGACATTTGTACATTTAGTACAGCAATGGAATTAACACTTTAGAACAGATAGTTAAGAAATTAAGCAACAGTTTGGGATATATAAACAAATAGCTCTT

AsnGlnSerSerGluValIrrAspProGluValIrrMetMetIrrSerPheAsnCysArgGluValIrrPhePheThrThrGluValIrrPheAsnAsnThrIrrArgLeuAsnMetIrrGlu 411
AATCAATCTTCAGAGGAGGACCCAGAAATTTGTAATGACAGCTTTTATTTAGAGGAGGATTTTCTACTGTAATACACAGCACTTTTAAATATACATGAGGCTTAAATACACTGAA

GluThrLysGluValAsnAspThrIrrIrrLeuProCysArgIrrLysGluValIrrAsnMetTrpGluValIrrGluValIrrValIrrAlaProProIrrGluValIrrSerCysSer 451
GGAAGTAAAGGAATGACACAATCATCTCCCATGTAGAAATAAACAAATATATACATGTGTCAGAGAGTAGGAAAGCAATGTATGCCCTCCCATTTGAGAGGAGCAATTAGTGTGTTCA

SerAsnIrrThrGluValLeuLeuValThrArgAspGluValIrrThrAsnValIrrAsnAspThrGluValIrrPheArgProGluValIrrLysPheMetArgAspAsnIrrArgSerGluValLys 491
TCAAAATTTACAGGCTGCTATTAAACAGAGAGATGTTGTTAGCAATGTAACTAATGACACGAGGCTTTCAGACCTGGAGGAGAGATATAGGAGCAATTTGGAGAGGATGAAATATATATAA

TyrLysValIrrLysIrrGluValProAsnSerValSer 7220
TATAAGTAATAAATTAATGACCAATTCGATATCTTGA

PKY Promoter

PKY Terminator

FIG. 11

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Nucleotide
positions
relative to
FIGURE 5.

MetIleAspLysAlaGlnGluGluHisGluLysTyrHisSerAsnTrp
 1 AGGXAAACAG:::ATGAT:GA:AAGGCACAA6AAGAACATGAGAAATATCACAGTAATTGG
 TCCXTTGTCT:::TACTA:CT:TTCCGTGTTCTTCTTGTACTCTTTATAGTGTCTTAACC

32 mbo11, 38 nla111,

3820 62 ArgAlaMetAlaSerAspPheAsnLeuProProValValAlaLysGluIleValAlaSer
 AGAGCCATGGCTAGTGTATTTAACCTGCCACCTGTAGTAGCAAAAGAAATAGTAGCCAGC
 TCTCGGTACCGATCACTAAAATTGGACGGTGGACATCATCGTTTTCTTTATCATCGGTCTG

66 nco1, 67 nla111, 118 nspBII pvu11, 119 alu1,

3880 122 CysAspLysCysGlnLeuLysGlyGluAlaMetHisGlyGlnValAspCysSerProGly
 TGTGATAAATGTCTAGCTAAAAGGAGAGCCATGTCATGGACAAGTAGACTGTAGTCCAGGA
 ACACATTTTACAGTCTGATTTTCTCTTCTGCTACGTACCTGTTCTGACATCAGGTCTCT

135 alu1, 151 nla111, 152 nsi1 ava3, 155 nla111, 164 acc1, 1
 76 apy1 bstXI ecor11 scrF1,

3940 182 IleTrpGlnLeuAspCysThrHisLeuGluGlyLysIleIleLeuValAlaValHisVal
 ATATGGCAACTAGATTGTACACATCTAGAAGGAAAAATTATCTGGTAGCAGTTCATGTA
 TATACGTTGATCTAACATGTGTAGATCTTCTTTTAAATAGGACCATCGTCAAGTACAT

198 rsa1, 205 xba1, 223 apy1 ecor11 scrF1, 236 nla111,

4000 242 AlaSerGlyTyrIleGluAlaGluValIleProAlaGluThrGlyGlnGluThrAlaTyr
 GCCAGTGGATATATAGAAGCAGAGATTATCCAGCAGAGACAGGGCAGGAAACAGCATAT
 CGGTACCTATATATCTTCTCTTCAATAAGGTCTCTCTGTCCCGTCTTTGTCTGTATA

263 xmn1,

4060 302 PheLeuLeuLysLeuAlaGlyArgTrpProValLysThrIleHisThrAspAsnGlySer
 TTTCTCTTAAATAGCAGGAAGATGGCCAGTAAAAACAATACATACAGACAATGGCAGC
 AAAGAGAATTTTAAATCGTCTTCTACCGGTCAATTTTGTATGTATGTCTGTTACCGTCTG

321 mbo11, 326 bal1 cfr1 hae1, 327 hae111, 357 bbv fnu4h1,

4120 362 AsnPheThrSerThrThrValLysAlaAlaCysTrpTrpAlaGlyIleLysGlnGluPhe
 AATTTACCCAGTACTACGGTTAAGGCCGCTGTTGTTGGGCAGGGATCAAGCAGGAATTT
 TTAAAGTGGTCTATGATGCCAATTCCGGCGGACAACCCGTCCTAGTTCGTCTTAA

366 hph, 371 sca1, 372 rsa1, 385 hae111, 386 fnu4h1 nsb11, 4
 05 bin1, 406 dpn1 sau3a,

4180 422 GlyIleProTyrAsnProGlnSerGlnGlyValValGluSerMetAsnAsnGluLeuLys
 GGCATTCCTACAAATCCCCAAAGTCAAGGAGTAGTAGAATCTATGAATAATGAATTAAAG
 CCGTAAGGGATGTTAGGGGTTTCAGTTCCTCATCATCTTAGATACTTATTACTTAATTTCT

423 bsm1, 458 hinf1,

4240 482 LysIleIleGlyGlnValArgAspGlnAlaGluHisLeuLysThrAlaValGlnMetAla
 AAAATTATAGGACAGGTAAGAGATCAGGCTGAACACCTTAAGACAGCAGTACAAATGGCA
 TTTTAATATCTGTCCATTCTCTAGTCCGACTTGTGGAATTCTGTCTCATGTTTACCGT

503 dpn1 sau3a, 518 afl11, 530 rsa1,

4300 542 ValPheIleHisAsnPheLysArgLysGlyGlyIleGlyGlyTyrSerAlaGlyGluArg
 GTATTTCATCCACAATTTTAAAGAAAGGGGGGATTGGGGGATACAGTGCAGGGGAAAGA
 CATAAGTAGGTGTTAAATTTTCTTTTCCCCCTAACCCCTATGTCACGTCCCCTTTCT

547 fok1, 557 sha111,

4360 602 IleValAspIleIleAlaThrAspIleGlnThrLysGluLeuGlnLysGlnIleThrLys
 ATAGTAGACATAATAGCAACAGACATACAACTAAAGAACTACAAAAGCAAATTACAAAA
 TATCATCTGTATTATCGTTGTCTGTATGTTTGATTTCTTGATGTTTTCTTTAATGTTTT

605 acc1,

662 IleGlnAsnPheArgValTyrTyrArgAspAsnLysAspProLeuTrpLysGlyProAla
 ATTCAAATTTTTCGGGTTTATTACAGGGACAACAAAGATCCCCTTTGGAAAGGACCAGCA

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4480 722 LysLeuLeuIrpLysGlyGlyGlyAlaValValIleGlnAspAsnSerAspIleLysVal
 AAGCTTCTCTGGAAAGGTGAAGGGGCAGTAGTAATAACAATAATAGTGACATAAAAGTA
 TCGAAGAGACCTTTCCACTTCCCCGTCATCATTATGTTCTATTATCACTGTATTTTCAT
 722 hind111, 723 alu1, 737 hph,
 4540 782 ValProArgArgLysAlaLysIleIleArgAspTyrGlyLysGlnMetAlaGlyAspAsp
 GTGCCAAGAAGAAAAGCAAAAATCATTAGGGGATTATGGAAAACAGATGGCAGGTGATGAT
 CACGGTTCTTCTTTTCGTTTTTAGTAATCCCTAATACCTTTTGTCTACCGTCCACTACTA
 789 mbo11, 833 hph,
 4600 842 CysValAlaSerArgGlnAspGluAspAM
 TGTGTGGCAAGTAGACAGGATGAAGATTAGTCGACGGAATTCTTTAGTAAACACC
 ACACACCGTTCATCTGTCTACTCCTAATCAGCTGCCCTTAAGAAATCATTTTGTGG
 852 acc1, 859 fok1, 863 mnl1, 871 acc1 hind11 sal1, 872 taq1
 , 878 ecor1,

FIGURE 12

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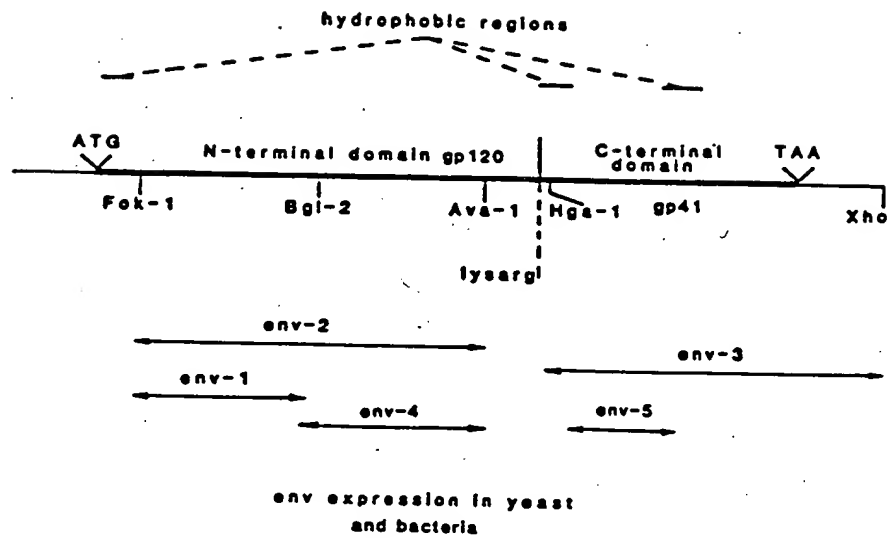


FIGURE 13

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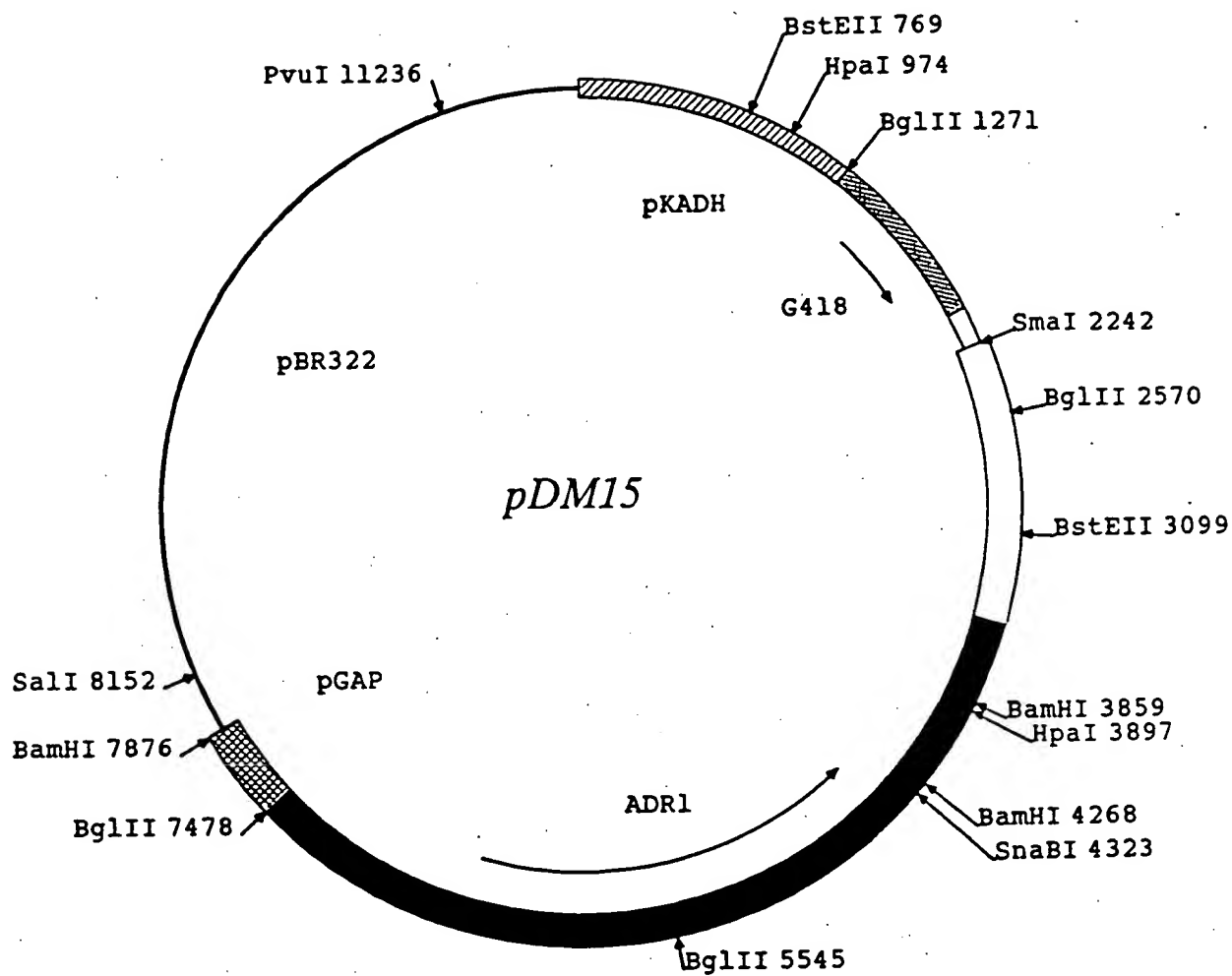


FIGURE 14

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- SCD
 MetAlaThrLysAlaValCysValLeuLysGlyAspGlyProValGlnGlyIleIleAsn
 1 CATGGCGACGAAGGCCGTGTGCTGCTGAAGGGCGACGGCCAGTGCAGGGCATCATCAAT
 CGCTGCTTCCGGCACACGCACGACTTCCCGCTCCGGTCACGTCCCGTAGTAGTAA

 PheGluGlnLysGluSerAsnGlyProValLysValTrpGlySerIleLysGlyLeuThr
 62 TTCGAGCAGAAGGAAAGTAATGGACCAGTGAAGGTGTGGGGAAGCATTAAAGGACTGACT
 AAGCTCGTCTTCCCTTCACTACCTGGTCACCTCCACACCCCTTCGTAAATTCCTGACTGA

 GluGlyLeuHisGlyPheHisValHisGluPheGlyAspAsnThrAlaGlyCysThrSer
 122 GAAGGCCCTGCATGGATTCCATGTTTCATGAGTTTGGAGATAATACAGCAGGCTGTACCACT
 CTTCCGGACGTACCTAAGGTACAAGTACTCAAACCTCTATTATGTCTGCGCATGGTCA

 AlaGlyProHisPheAsnProLeuSerArgLysHisGlyGlyProLysAspGluGluArg
 182 GCAGGTCCCTCACTTTAATCCTCTATCCAGAAAACACGGTGGGGCCAAAGGATGAAGAGAGG
 CGTCCAGGAGTGAAATAGGAGATAGGTCTTTTGTGCCACCCGGTTTCTACTTCTCTCC

 HisValGlyAspLeuGlyAsnValThrAlaAspLysAspGlyValAlaAspValSerIle
 242 CATGTTGGAGACTTGGGCAATGTGACTGCTGACAAAGATGGTGTGGCCGATGTGTCTATT
 GTACAACCTCTGAACCCGTACACTGACGACTGTTTCTACCAACCCGCTACACAGATAA

 GluAspSerValIleSerLeuSerGlyAspHisCysIleIleGlyArgThrLeuValVal
 302 GAAGATTCTGTGATCTCACTCTCAGGAGACCATTGCATCATTGGCCGCACACTGGTGGTC
 CTTCTAAGACACTAGAGTGAGAGTCTCTGGAACGTAGTAACCGGCTGTGACCACCG

 HisGluLysAlaAspAspLeuGlyLysGlyGlyAsnGluGluSerThrLysThrGlyAsn
 362 CATGAAAAGCAGATGACTTGGGCAAGGTGGAATGAAGAAAGTACAAAGACAGGAAC
 GTACTTTTTCGTCTACTGAACCCGTTTCCACCTTACTTCTTCTCATGTTTCTGTCTCTTG

 ENV 53
 AlaGlySerArgLeuAlaCysGlyValIleGlyIleAlaMetAlaIleGluAlaGlnGln
 422 GCTGGAAGTCGTTTGGCTTGTGTGTAATGGGATCGCCATGGCTATCGAAGCTCAACAA
 CGACCTTCAGCAAAACCGAACACCATTAACCCCTAGCGGTACCGATAGCTTCGAGTTGTT
 461
 HisLeuLeuGlnLeuThrValTrpGlyIleLysGlnLeuGlnAlaArgValLeuAlaVal
 482 CACTTGCTGCAGTTGACCGTTTGGGTATCAAGCAGTTGCAGGCTAGAGTTTGGCTGTT
 GTGAACGACGTCACCTGGCAAACCCCATAGTTCGTCAACGTCGGATCTCAAAACCGACAA

 GluArgTyrLeuArgAspGlnGlnLeuLeuGlyIleTrpGlyCysSerGlyLysLeuIle
 542 GAAAGATACCTTGAGAGATCAACAAATTGTTGGGTATCTGGGGTGTCTGGTAAGTTGATT
 CTTTCTATGAATCTCTAGTTGTTAAACAACCCATAGACCCCAACAGACCATTCAACTAA

 CysThrThrAlaValProTrpAsnAlaSerTrpSerAsnLysSerLeuGluAspIleTrp
 602 TGTAACCACCGTGTTCCTGGAAACGCTTCTTGGTCTAACAAGTCTTGGAAAGACATCGG
 ACATGGTGGCGACAAGGGACCTTGGGAAGAACAGATTGTTTCAGAAACCTTCTGTAGACC

 AspAsnMetThrTrpMetGlnTrpGluArgGluIleAspAsnTyrThrAsnThrIleTyr
 662 GACAACATGACCTGGATGCAATGGGAAAGAGAAATCGACAACACCAACACCATCTAC
 CTGTTGTACTGGACCTACGTTACCTTTCTCTTAGCTGTGTGATGTTGTTGTTAGATG

 ThrLeuLeuGluGluSerGlnAsnGlnGlnGluLysAsnGluGlnGluLeuLeuGluLeu
 722 ACCCTGTTGGAGGAATCTCAAAACCAAGAAAAGAACGAACGAAGAAATTGTTGGAAATG
 TGGAACAACCTCCTTAGAGTTTGGTTGTTCTTTCTTCTGTTGTTCTTAACAACCTTAAC

 AspLysTrpAlaSerLeuTrpAsnTrpPheSerIleThrAsnTrpAM
 782 GACAAGTGGGCAAGCTTGTGGAACTGTTCTCTATCACCAACTGGTAG
 CTGTTACCCGTTTGAACACCTTGACCAAGAGATAGTGGTTGACCATCAGCT

Translated Mol. Weight = 30414.22

FIGURE 15

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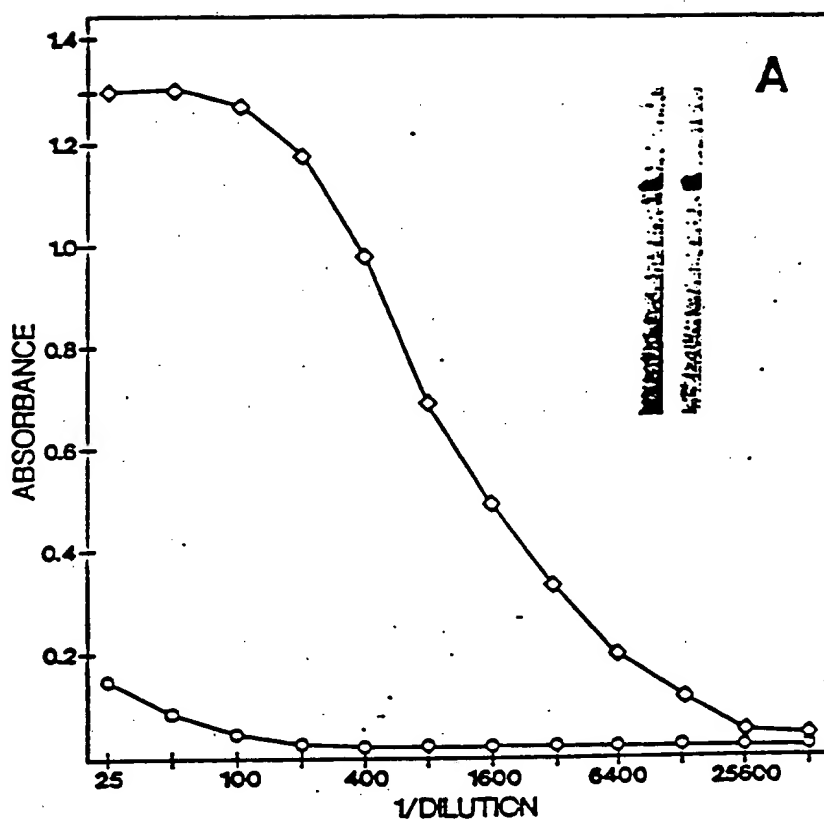


FIGURE 16

1 of 2

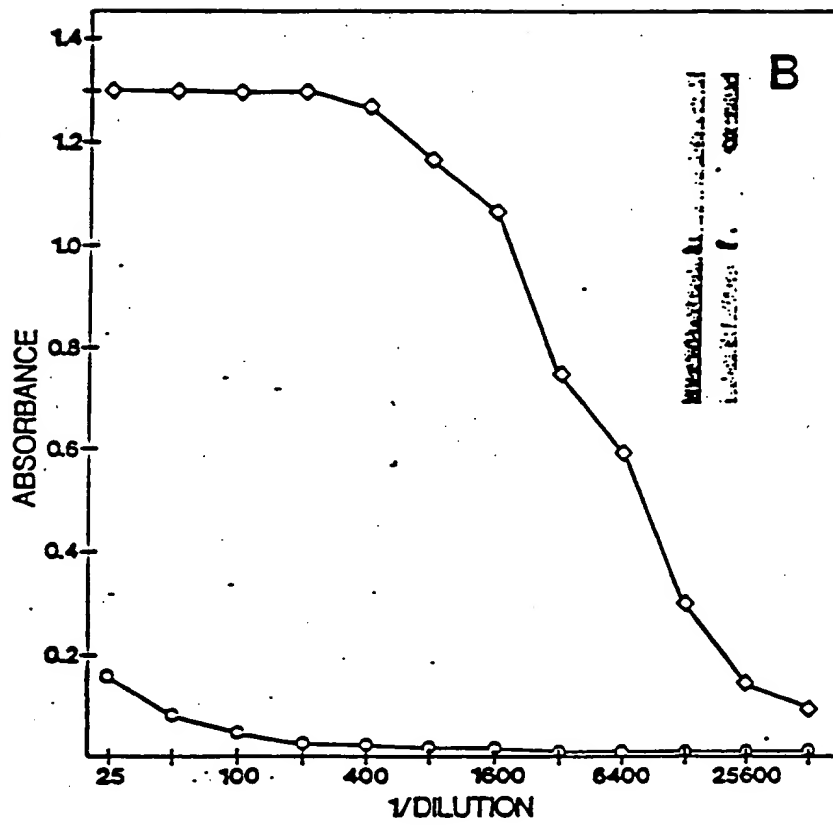


FIGURE 16

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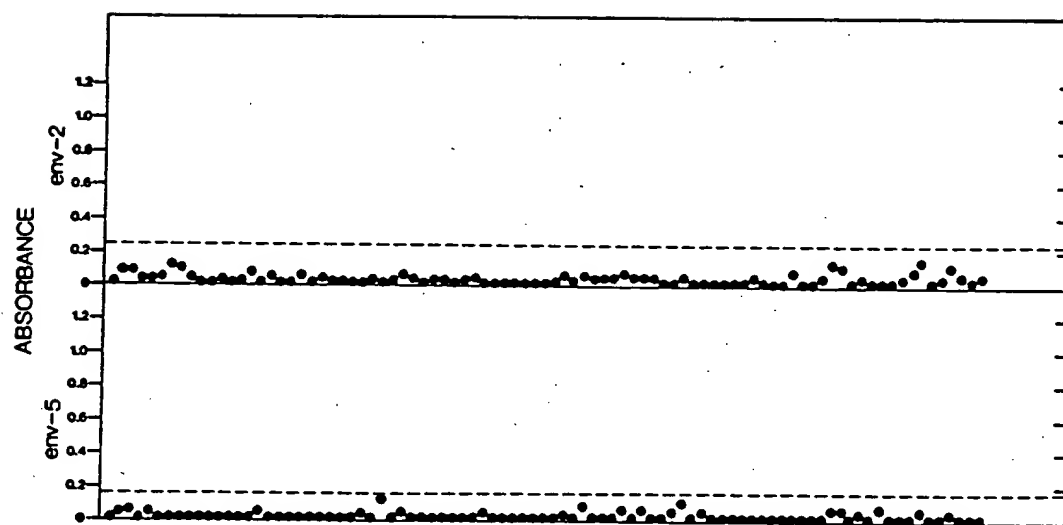


FIGURE 17

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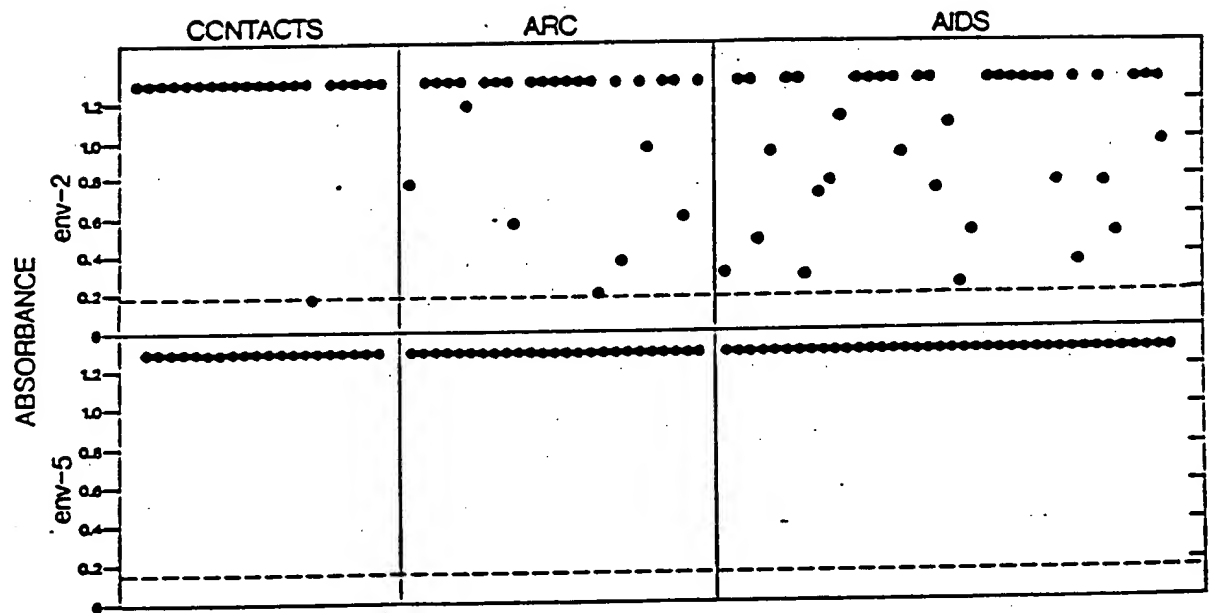


FIGURE 18



FIGURE 19

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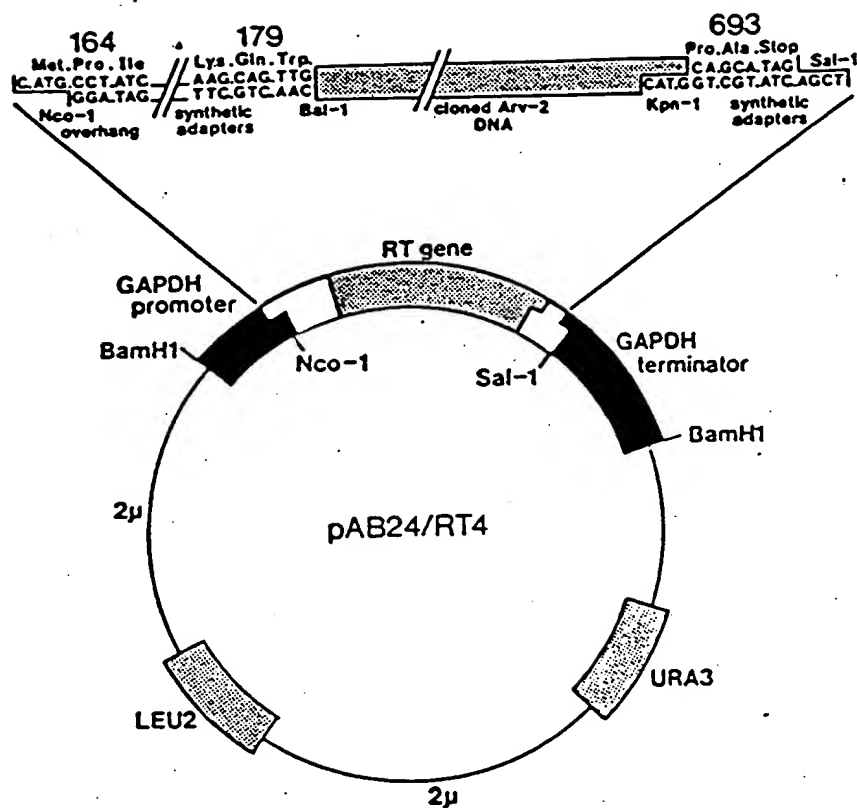


FIGURE 20

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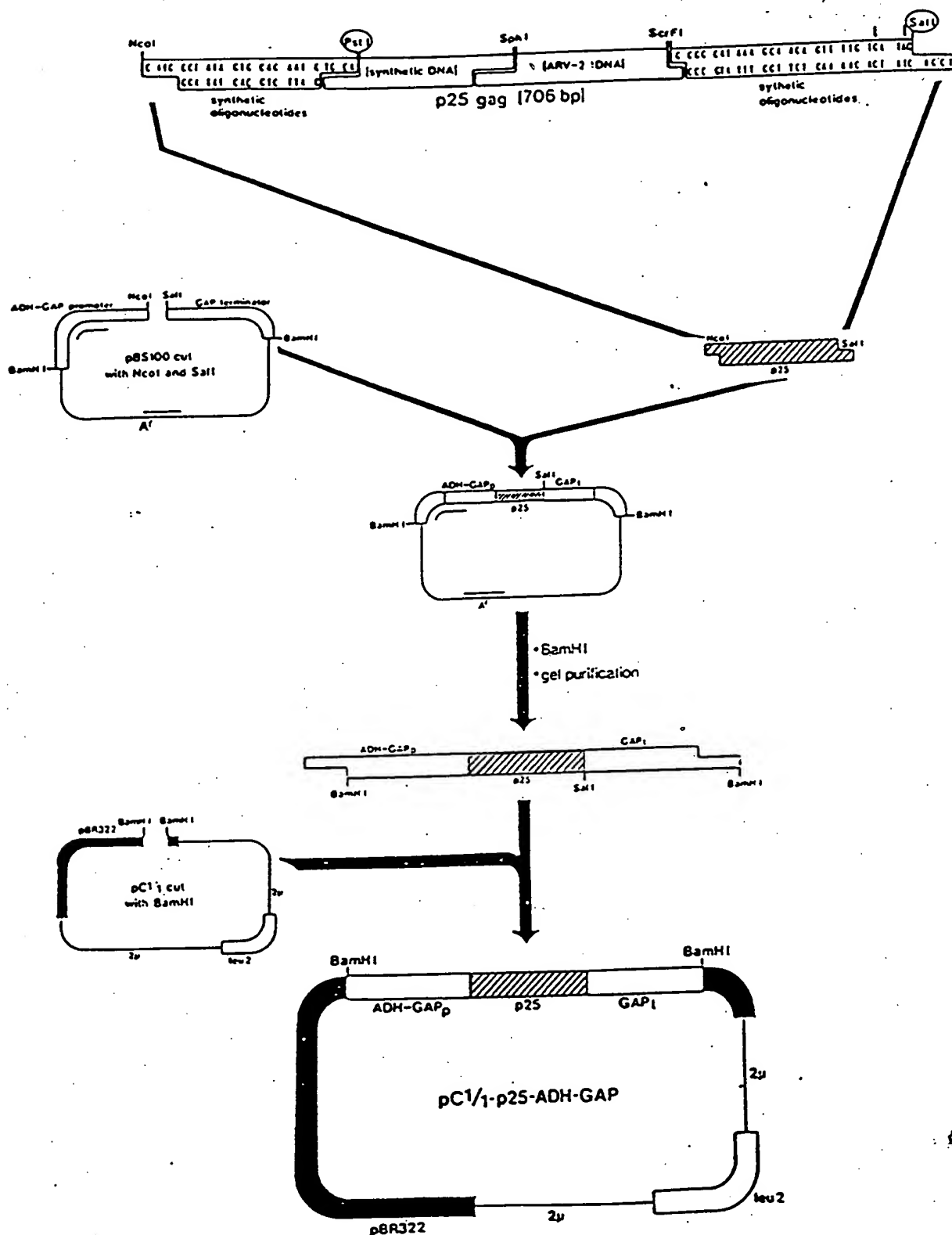


FIGURE 21

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1 10
Met Pro Ile Val Gln Asn Leu Gln Gly Gln Met Val His Gln
C ATG CCT ATA GTG CAG AAT CTG CAG GGG CAA ATG GTA CAT CAG

20
Ala Ile Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Val Glu
GCC ATA TCA CCT AGA ACT TTA AAT GCT TGC GTA AAA GTA GTA GAA

30 40
Glu Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu
GAA AAG GCT TTC AGC CCA GAA GTA ATA CCC ATG TTT TCA GCA TTA

50
Ser Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr
TCA GAA GGA GCC ACC CCT CAA GAT TTA AAC ACC ATG CTA AAC ACA

60 70
Val Gly Gly His Gln Ala Ala Met Gln Met Leu Lys Glu Thr Ile
GTG GGG GGA CAT CAA GCA GCC ATG CAA ATG TTA AAA GAG ACT ATC

80
Asn Glu Glu Ala Ala Glu Trp Asp Arg Val His Pro Val His Ala
AAT GAG GAG GCT GCC GAA TGG GAT AGA GTG CAT CCA GTG CAT GCA

90 100
Gly Pro Ile Ala Pro Gly Gln Met Arg Glu Pro Arg Gly Ser Asp
GGG CCT ATT GCA CCA GGC CAA ATG AGA GAA CCA AGG GGA AGT GAC

110
Ile Ala Gly Thr Thr Ser Thr Leu Gln Glu Gln Ile Gly Trp Met
ATA GCA GGA ACT ACT AGT ACC CTT CAG GAA CAA ATA GGA TGG ATG

120 130
Thr Asn Asn Pro Pro Ile Pro Val Gly Glu Ile Tyr Lys Arg Trp
ACA AAT AAT CCA CCT ATC CCA GTA GGA GAA ATC TAT AAA AGA TGG

140
Ile Ile Leu Gly Leu Asn Lys Ile Val Arg Met Tyr Ser Pro Thr
ATA ATC CTG GGA TTA AAT AAA ATA GTA AGA ATG TAT AGC CCT ACC

150 160
Ser Ile Leu Asn Ile Arg Gln Gly Pro Lys Glu Pro Phe Arg Asp
AGC ATT CTG GAC ATA AGA CAA GGA CCA AAG GAA CCC TTT AGA GAT

170
Tyr Val Asp Arg Phe Tyr Lys Thr Leu Arg Ala Glu Gln Ala Ser
TAT GTA GAC CGG TTC TAT AAA ACT CTA AGA GCC GAA CAA GCT TCA

180 190
Gln Asp Val Lys Asn Trp Met Thr Glu Thr Leu Leu Val Gln Asn
CAG GAT GTA AAA AAT TGG ATG ACA GAA ACC TTG TTG GTC CAA AAT

200
Ala Asn Pro Asp Cys Lys Thr Ile Leu Lys Ala Leu Gly Pro Ala
GCA AAC CCA GAT TGT AAG ACT ATT TTA AAA GCA TTG GGA CCA GCA

210 220
Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln Gly Val Gly Gly
GCT ACA CTA GAA GAA ATG ATG ACA GCA TGT CAG GGA GTC GGG GGA

230 232
Pro Gly His Lys Ala Arg Val Leu OP
CCC GGG CAT AAA GCA AGA GTT TTG TGA TAG

Translated Mol. Weight = 25700.75

FIGURE 22

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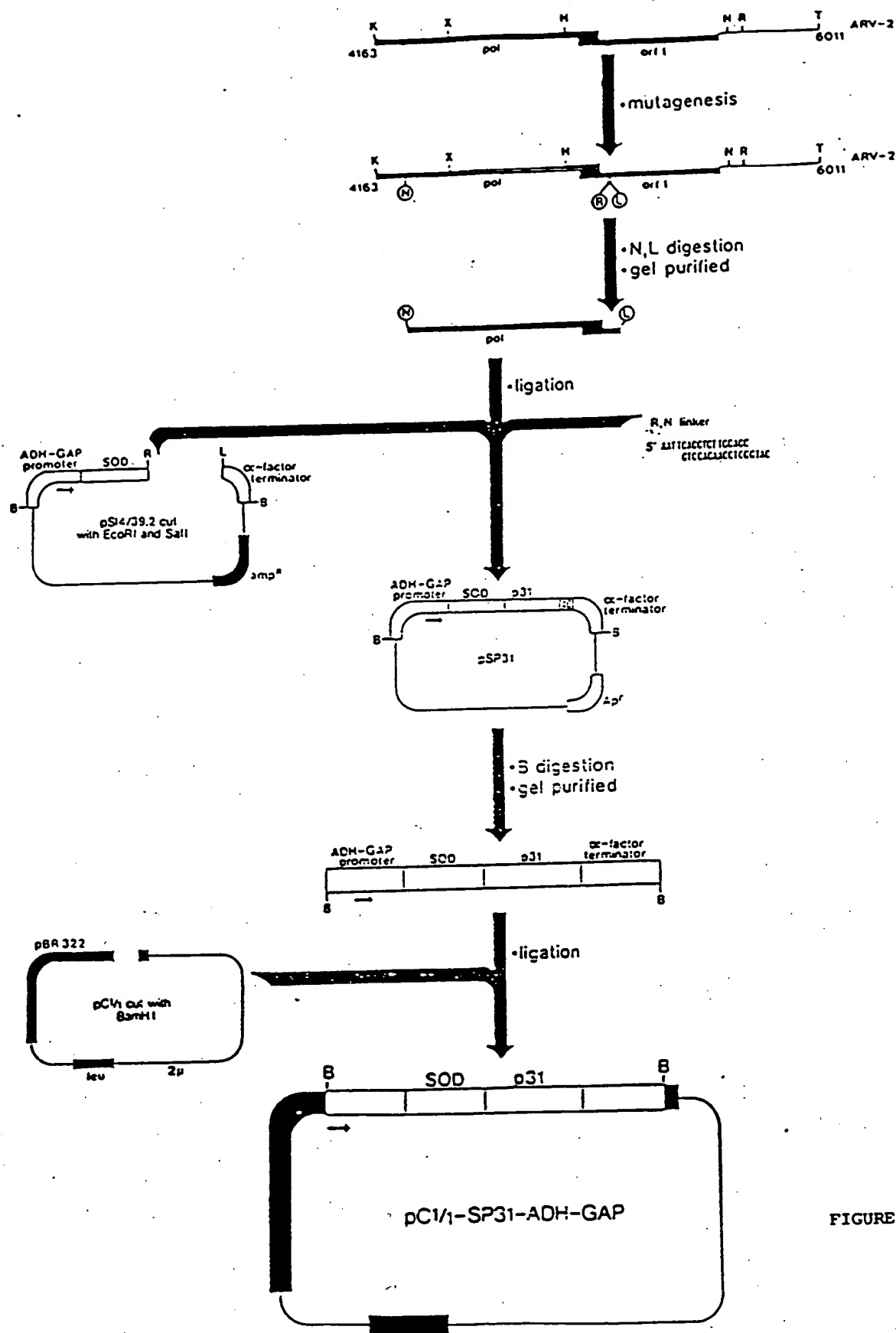


FIGURE 23

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500 -->
MetAlaThrLysAla
ATGGCTACAAAGGCT
TACCGATGTTTCCGA

1383 ValCysValLeuLysGlyAspGlyProValGlnGlyIleIleAsnPheGluGlnLysGlu
GTTTGTGTTTTGAAGGGTGACGGCCAGTTCAGGTATTATTAACTTCAGCAGAGAAGGAA
CAAAACACAAACCTTCCCACTGCCGGGTCAAGTTCATAATAATTGAAGCTCGTCTTCCTT

1443 SerAsnGlyProValLysValTrpGlySerIleLysGlyLeuThrGluGlyLeuHisGly
AGTAATGGACCACTGAAGGTGTGGGGAAGCATTAAAGGACTGACTGAAGGCCCTGCATGGA
TCATTACCTGGTCACTTCCACACCCCTTCGTAATTTCTGACTGACTTCGGGACGTACCT

1503 PheHisValHisGluPheGlyAspAsnThrAlaGlyCysThrSerAlaGlyProHisPhe
TTCCATGTTTCATGAGTTTGGAGATAATACAGCAGGCTGTACCACTGCAGGTCTCACTTT
AAGGTACCAAGTACTCAACCTCTATTATGTGTCGTCGACATGGTCAGCTCAGGAGTGA

1563 AsnProLeuSerArgLysHisGlyGlyProLysAspGluGluArgHisValGlyAspLeu
AATCCTCTATCCAGAAAACACGGTGGGCCAAAGGATGAAGAGAGGCATGTTGGAGACTTG
TTAGGAGATAAGTCTTTTGTGCCACCCGGTTTCTACTTCTCTCCGTACAACCTCTGAAC

1623 GlyAsnValThrAlaAspLysAspGlyValAlaAspValSerIleGluAspSerValIle
GGCAATGTGACTGCTGACAAAGATGGTGTGGCCGATGTGTCTATTGAAGTCTGTGATC
CCGTACACTGACGACTGTTTCTACCACACCGGCTACACAGATAACTTCTAAGACACTAG

1683 SerLeuSerGlyAspHisCysIleIleGlyArgThrLeuValValHisGluLysAlaAsp
TCACTCTCAGGAGACCATTCATCATTGGCCGACACTGGTGGTCCATGAAAAGCAGAT
AGTGAGAGTCTCTGTAACGTAGTAACCGGCGTGTGACCACCAAGTACTTTTTCTGCTA

1743 AspLeuGlyLysGlyGlyAsnGluGluSerThrLysThrGlyAsnAlaGlySerArgLeu
GACTTGGGCAAAAGTGGAAATGAAGAAAGTACAAAGACAGGAAACCTGGGAATCTTTG
CTGAACCCGTTTCCACCTTACTTCTTTCTATGTTTCTGTCCTTTGCGACCTTCAGCAAC

1803 AlaCysGlyValIleGlyIleAlaGlnAsnSerGlyValGlyAlaMetAlaMetAlaSer
GCTTGTGGTGAATTTGGGATCGCCAGAAATTCAGGTGTTGGAGCCATGGCCATGGCTAGT
CGAACACCACATTAAACCTAGCGGGTCTTAAGTCCACAACCTCGGTACCGGTACCGATCA

1863 AspPheAsnLeuProProValValAlaLysGluIleValAlaSerCysAspLysCysGln
GATTTTAACTGCCACCTGTAGTAGCAAAAGAAATAGTAGCCAGCTGTGATAAATGTGAG
CTAAATTTGGACGGTGGACATCATCGTTTTCTTTATCATCGGTGACACTATTACAGTC

1923 LeuLysGlyGluAlaMetHisGlyGlnValAspCysSerProGlyIleTrpGlnLeuAsp
CTAAAGGAGAGGACCATGCATGGACAAGTAGACTGTAGTCCAGGAATATGGCACTAGAT
GATTTTCTCTCGGTACGTACCTGTTCTCATCTGACATCAGGTCTTATACCTTGTATCTA

1983 CysThrHisLeuGluGlyLysIleIleLeuValAlaValHisValAlaSerGlyTyrIle
TGTACACATCTAGAAGGAAAAATTATCTTGGTAGCAGTTCTGTAGCCAGTGGATATATA
ACATGTGTAGATCTTCTTTTTAATAGGACCATCGTCAAGTACATCGGTCACTATATAT

2043 GluAlaGluValIleProAlaGluThrGlyGlnGluThrAlaTyrPheLeuLeuLysLeu
GAAGCAGAAGTATTTCAGCAGAGACAGGGCAGGAACAGCATATTTCTCTAAATTA
CTTCSTCTTCAATAAGGTCTGTCTGTCCCGTCTTGTGCTATAAAGAGAATTTAAT

2103 AlaGlyArgTrpProValLysThrIleHisThrAspAsnGlySerAsnPheThrSerThr
GCAGGAAGATGGCCAGTAAAAACAATACATACAGACAATGGCAGCAATTCACCACTACT
CGTCTTCTACCGGTCATTTTTGTATGTATGTCTGTTACCGTCTGTTAAAGGTGATCA

2163 ThrValLysAlaAlaCysTrpTrpAlaGlyIleLysGlnGluPheGlyIleProTyrAsn
ACGGTTAAGGCCGCTGTTGGTGGCAGGGATCAAGCAGGAATTTGGCATTCTCTACAAT
TGCCAATTCGGGCGGACAACCAACCCGTCCTAGTTCTGTCCTTAAACCGTAAGGGATGTTA

2223 ProGlnSerGlnGlyValValGluSerMetAsnAsnGluLeuLysLysIleIleGlyGln
CCCCAAAGTCAAGGAGTAGTAGAATCTATGAATAATGAATTAAGAAAAATTATAGGACAG
GGGTTTCACTTCTCATCTTAGATACCTTATTACTTAAATTTCTTTAATATCTGTGTC

2283 ValArgAspGlnAlaGluHisLeuLysThrAlaValGlnMetAlaValPheIleHisAsn
GTAAGAGATCAGGCTGAACACCTTAAGACAGCAGTACAAATGGCAGTATTCTCCACAAT
CATCTCTAGTCCGACTTGTGAATTTCTGTCGTATGTTTACCGTCATAAGTAGGTGTTA

2343 PheLysArgLysGlyGlyIleGlyGlyTyrSerAlaGlyGluArgIleValAspIleIle
TTTTAAAGAAAAGGGGGGATTGGGGGATACAGTGCAGGGGAAAGAAATAGTAGACATAATA
AAATTTTCTTTTCCCCCTAACCCCTATGTACGTCCTCTTCTTATCATCTGTATTAT

2403 AlaThrAspIleGlnThrLysGluLeuGlnLysGlnIleThrLysIleGlnAsnPheArg
GCAACAGACATACAACTAAAGAACTACAAAAGCAAATACAAAAATTCAAAATTTTCGG
CSTTGTCTGTATGTTGATTTCTGATGTTTCTGTTAATGTTTAAAGTTTTAAAGGCC

2463 ValTyrTyrArgAspAsnLysAspProLeuTrpLysGlyProAlaLysLeuLeuTrpLys
GTTTATTACAGGGCAACAAAGATCCCCCTTTGGAAAGGACCAAGGCTTCTCTGGAAG
CAAAATATGTCCTGTTGTTTCTAGGGGAAACCTTCTGCTGTTTGAAGAGACCTTT

2523 GlyGluGlyAlaValValIleGlnAspAsnSerAspIleLysValValProArgArgLys
GGTGAAGGGGCACTAGTAATAACAGATAATAGTGACATAAAAGTAGTGCCAAAGAAAA
CCACTTCCCCGTATCATTTATGTTCTATTATCACTGTATTTTCTATCACGGTCTTCTTTT

2583 AlaLysIleIleArgAspTyrGlyLysGlnMetAlaGlyAspAspCysValAlaSerArg
GCAAAATCATTAGGCATTATGGAAAAACAGATGGCAGGTGATGTTGTGTGGCAAGTAGA
CGTTTTTAGTAATCCCTAATACCTTTTGTCTACCGTCCACTACTAACACACCGTTCATCT

2643 GlnAspGluAspAsn
CAGGATGAGGATTAG
GTCTACTCTAATC

FIGURE 24

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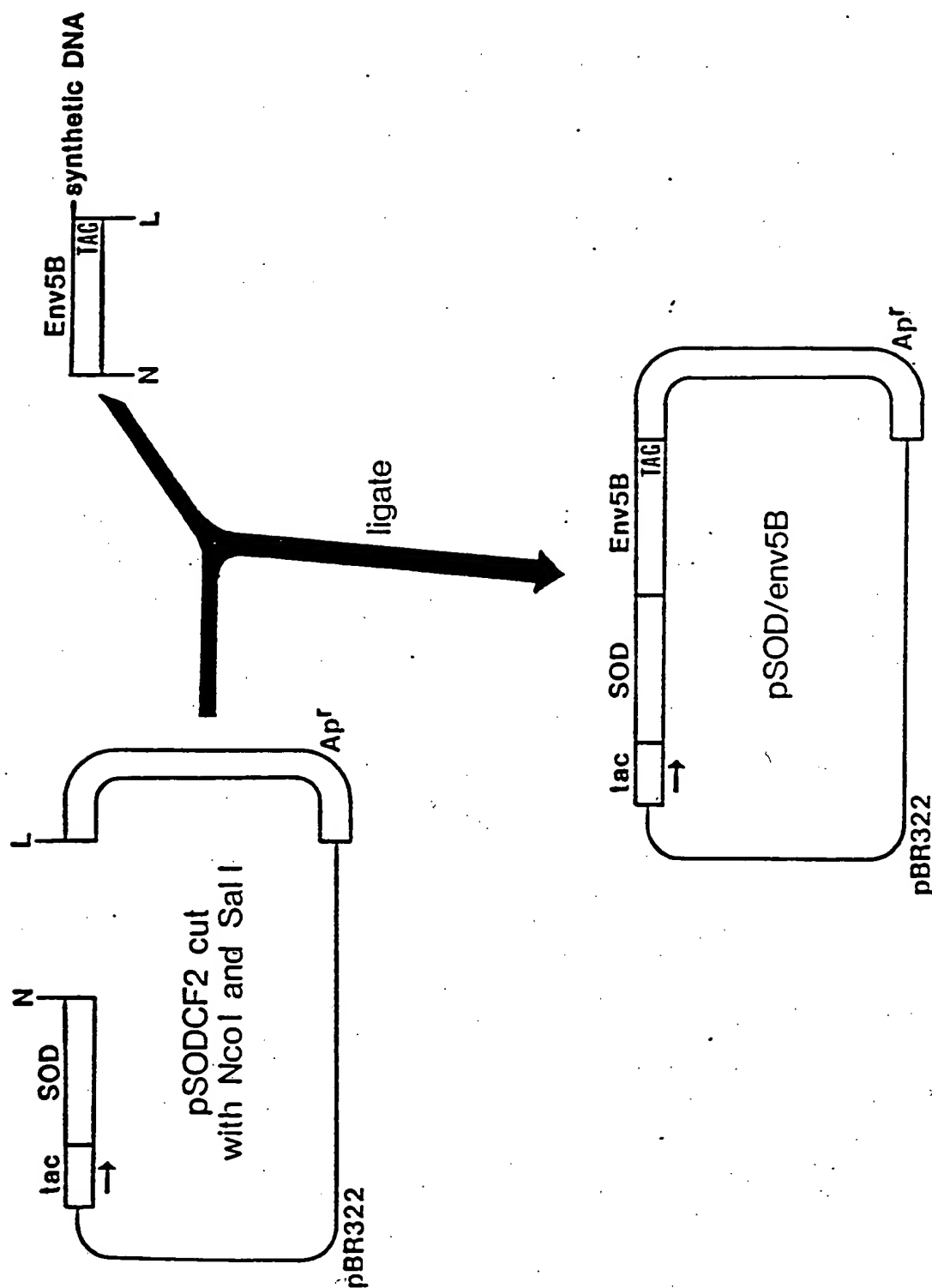


FIGURE 25

Sequence of SOD/env-4

1-300

1	HebAlaThryaLaVaLyCyVaLeuWedyedlyAepdyIpyroValodIdelyIleleAen CATGCGAGAGAGTGGCTGGCTGAGAGGGCGAGCGCGAGTGGCGGGCATGATCAAT CGCTGTTCGGGCGACAGAGAGTTCGCGCTGGCGGGGTACAGTCCGCTGGCTGATCTTA
62	PhedIdInlyedIuSerAendlypyroValyVaLtpdyIserIlelylelyleuTh TTGAGGCAAGAGAGTAAAGTAAAGAGTGAAGGTGGAGAACATTAAGAGTCACT AAGCTGTCTTCCTTAACTTAAGTCTGCTACTTCACACACCCCTTGGTAAATTCTCTGCTGA
22	GluUdyLeuIdelyPheHleVaLHleIduphedlyAepAenThleAledlyCyethuSer GAAGGCTTCAGTGGATTCATGATTCATGAGTTGTAGATTAATACAGAGGCTGACAGT CTTTCGGAGGCTGAGTACCTTAAGGTTGACAGTACTCAAACTCTTATGTTGCTGCAGCATGTCA
82	AlledyProthleAenPLeuSerAendlyAethleIdyIpyrolyAepdyIdelyuTh GCAGCTCTCACTTTAACTCTCTATCCAGAAACAGGTGGCGGCAAGCATGACAGGAG CGTCCAGGAGTGAATTAGGAGATAGTCTTTTGTGGCCACCGCGTTCTTACTTCTCTCC
142	HisValolyleAepLeuIdyAenValThrAlaAeplyAepdyIyAlaAeplyAserIle CATGTTGGAGATCTGGCATGATGAGTGGAGAGATGAGTGTGGCGCATGTGTCTATT GTACAGCTCTGACCGCTTACTACTGACGACTGTGTTCTTACACACCGGCTACACAGATAA
202	GluAepSerValIleSerLeuAendlyAepHleCyelleIdelyAethuThLeuValal GAGATCTGTGATCTACTCTCAGGAGCAATGCTCATATCCGCGAGCTGGCT CTTCTTACAGACTAGTGGAGAGTCTCTGTTAGTAAAGTAAACCGCGTGTGGACACG
262	HisUdyAleAepAepLeuIdyIyAendlyIuSerThyethuThlyAen CATGAAGAAGAGTATCTGGGCAAGGTGGAGTGAATGAGAAAGTACAAAGCAGGAAAC GTACTTTTCTGCTACTGACCGCGTTTCCACCTTACTTCTTCTTCTTCTTCTGCTCTTTC
322	AlledySerArgLeuAlCyedlyValIledlyIleAethuThlyValIleAethuSer GCTGGAGTCTTGTGCTGTGTGTGTATTTGGTATCCCATGGAGGTGGTAAATTAGATCT CGACTTCAGCAACCGACACACACATTAACCTTAGGCGGTAACTCCATCATTAATCTGA
382	AepAenPheThAenAenAlaIyAenCATTATleValleIdnLeuAendlyuSerValleIle GACATCTACAGAACATCTTAACACATTAATAGTACAGCTGAATCATCTGTACACAAIT CTGTTAAGTGTCTTACGATTTGGTATATCATATGCGACTTACTTAGACATCGTTAA
442	AenCyethuThArgpAenAenThrArglyAserIleIyIledIpyroIdyAethuAla AAGCTGTACAGGACACACACATCAAAAGTAAAGTATATATATATATATATATATATAT TTGACCTTGTGGGTGTGTGTGTATGTTCTTTTATATAGATATATATGCTGGTCCCTCTGT
502	PheHleThurThlyArgyleIdelyAepIleAethuThleAethuAenIleSerArg TTTCTATACAGAGAGATTAATATAGATATATAGAAAGACATNTGTTAACTATATAGTA AAAGTATGTGTCTCTCTTATATCTCTATATCTTTTCTGGTGAACATCTGATATCT
562	GACATGTGAATACCTTTTAGACAGATGTTTAAATATATAGAGACAGCTGTGGAT CGTGTTCCTTATGTGAATCTGTCTGTCTATCTTATATATATATCTCTCTCTCAACCGCTTA
622	AenlyAethuThleValPheAendInSerSerCAGlyAeprodIdyIleValHleHleAser ATAAACAATGTCTTATATCACTCCGAGGAGGAGCGAGAAATGTTAATCTACAGT TTATTTGTGTATACAAATATGTAGGAGTCCCTCCCTGGCTTTTACATTAAGTGTCA
682	PheAenCyethuArgdlyIuPhePheThyCyAenThurThIdInLeuPheAenThurThp TTTTATGTAGAGGGAATTTCTACTGTCTGATACACACACACCTGTGATATATACATG AATTTATACATCTCCCTCTTAAAGATGATATATGTGTGTGCAAAATATATATATGAC
742	ArgLeuAenHleThurGluGlyThryedlyAenAepThrIleIleLeuPheCyAethuIle TTCAATTAATACATGATGATCAATTAAGATATATACATCAATCTCCCATATATATAT TCCAAATGTGATATCTCTAT

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902	LysGlnIleIleAsnMetTrpGlnGluValGlyIysAlaMetIyrAlaProProlIleGly AlaMetAlaTATAAATGATGGCCAGGAGATGGGAAAGCATATGATGCGGCTCCCATATGGA TTTGTTATATATATTTATGATACCGCTCTTCATCTCTTTCGTTTACATATACGGCCAGGGTAACCTG
962	GlyGlnIleSerCysSerAsnIleThrGluLeuLeuLeuLeuArgLeuArgLeuIleCysIyr GGCAAAATTATGTCATCATCATANTATACAGGCTGCTCTTTAAACAGAGCATGCTGGTACCA CCTGTTTATATCAACAAGTAGTTTATATATGTCGCCAGAGTCTGCTCTCTACCCACCATGT
1022	AsnValThrAsnAsnGluValAlaPheArgProIleGlyIleIyrAspMetArgAlaPleuTrp AATGTACTATATATGACACGAGGTCTTCAGACCTGTGGAGGAGATATGAGCAACAATTCG TTTCATTTGATTACTGTGGCTCCAGAGTCTGGACACTGCTGCTCTATACTCTCTGTATTAAC
1082	ArgSerGluLeuLeuIyrCysIyrIysValIleAlaIleGluIleProLeuGlyIleIleAlaProThr AGAGTGAATATATTAATATATTAAGTATTAATATTAAGTATTCATTCGATACAGCCACCC TCTTCACCTTAATATATTTATNTTTCNTTNTTTTTAACTGTGTTATTCCTTATCTTGGGTGG
1142	LysAlaIysArgCysValGlnIleArgGluIysArgProP AGGCAAAAGAGAGAGGTGGTCCAGAGAGCAAAAGATGATGATAGCTTTG TTGCTGTTCTCTCTCCACAGCTCTCTCTTTTCTTCTACTCTACTCTGCAAGCT

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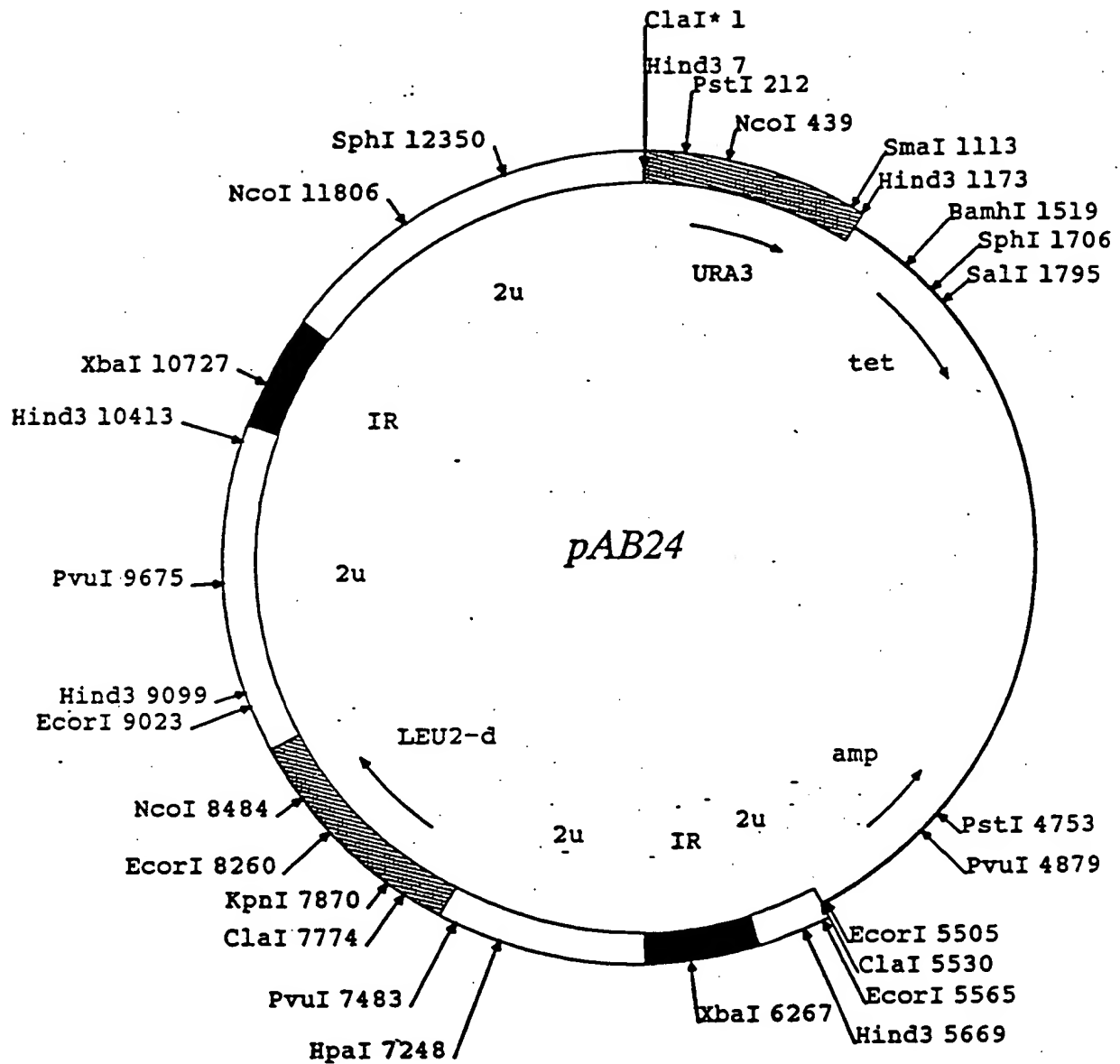


FIGURE 27

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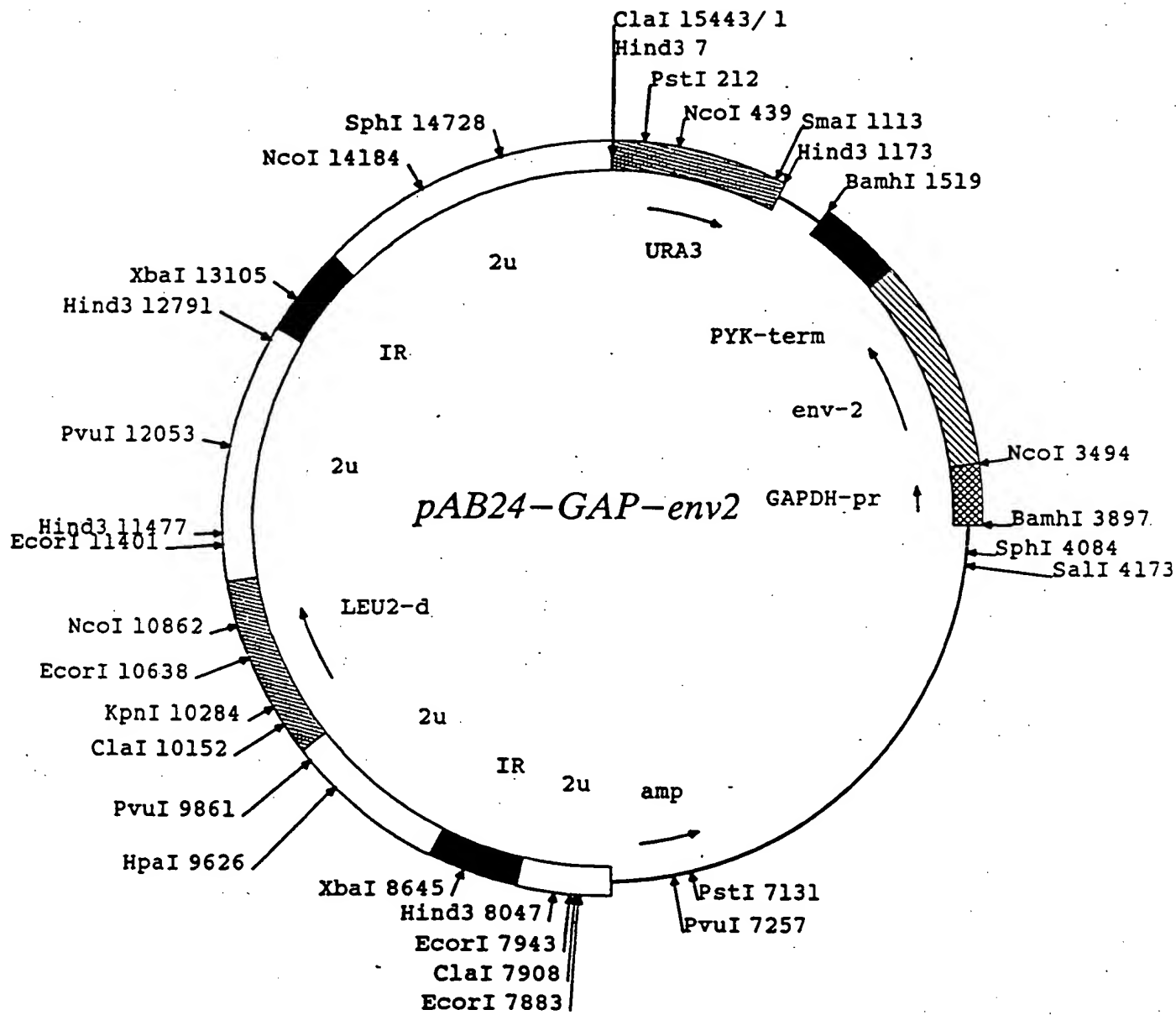


FIGURE 28

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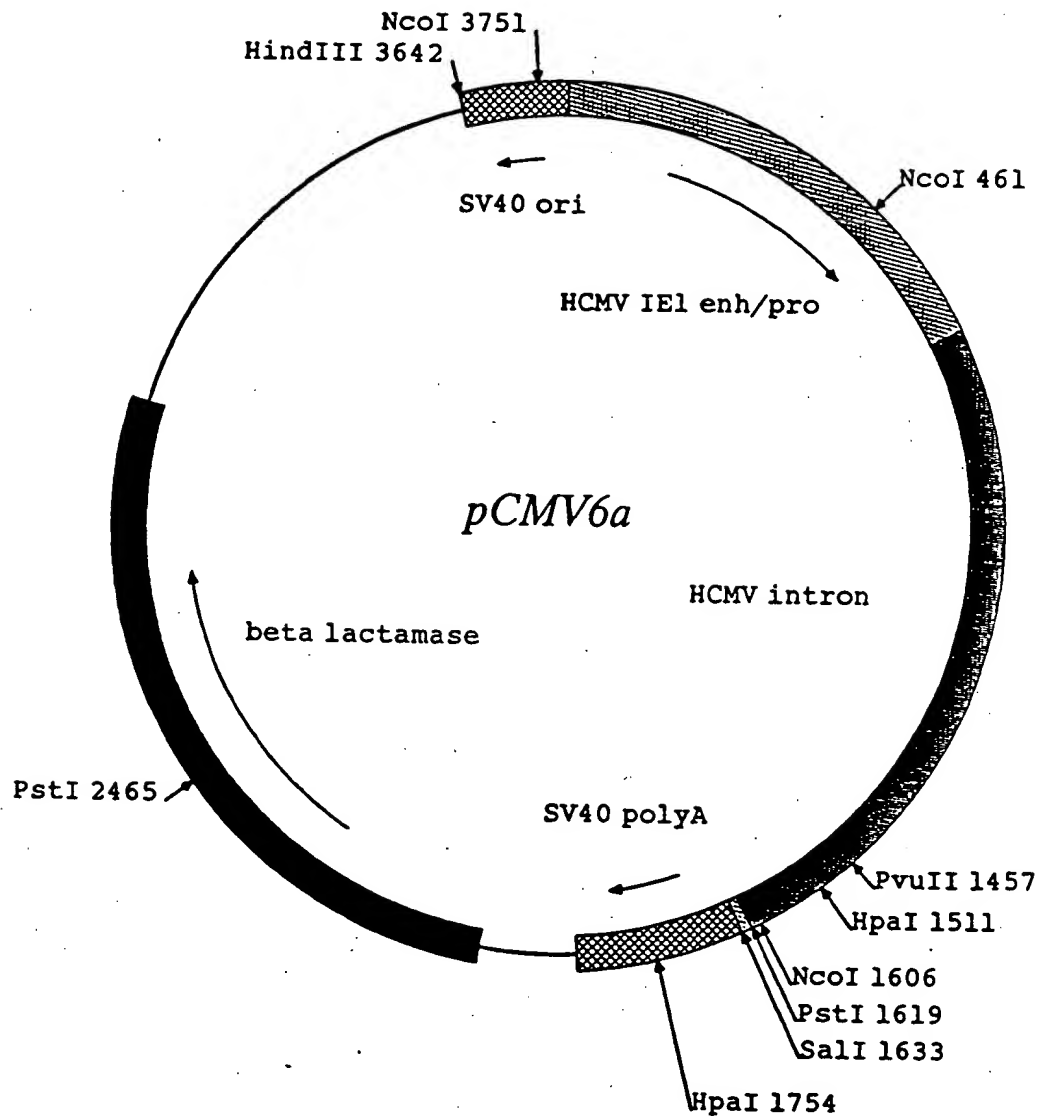


FIGURE 29

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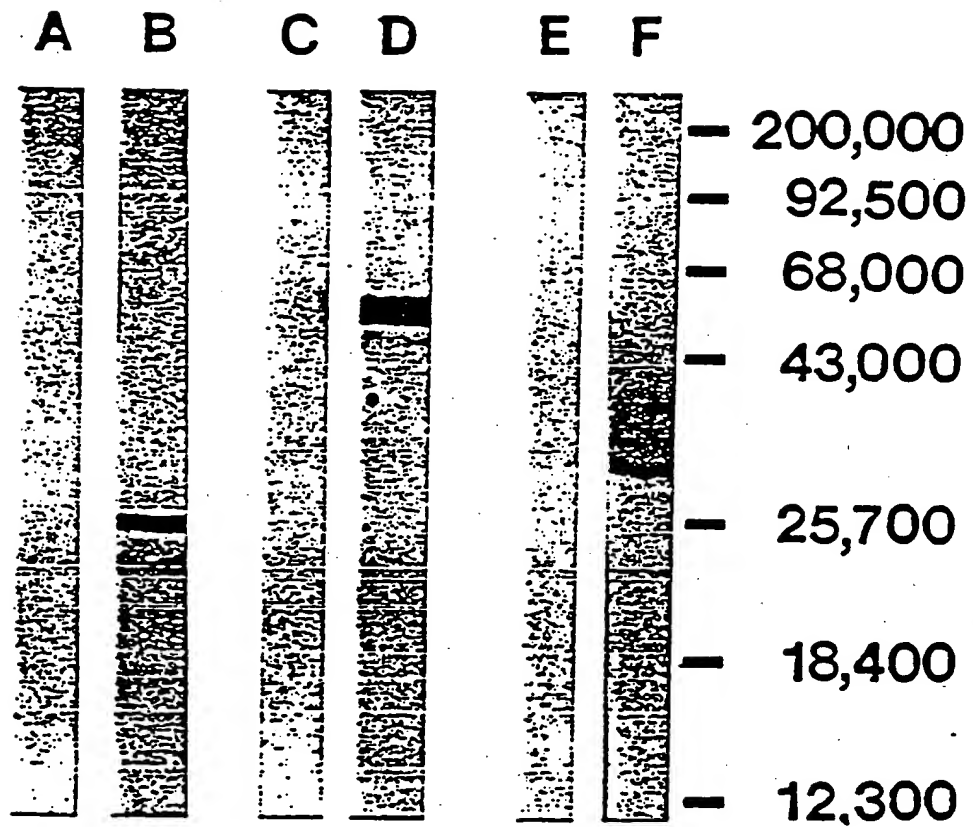


FIGURE 30